

FIG. 1A

AGGGGGCGCGGTGGATGCGGCGGAGCTGGAAGCCTCGAGCAGCGGCGCCTTCT
 CTGGCCCCGGCGCATATGGCTTGAAGAGCCGTGCCACCCAGTGGCCCCACTGCCCCA
 1 Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg
 ATG GAT CCA CCA CTG AAC TCC TCG TCG TCG TCG TCG TCG TCG TCG TCG
 10
 * 20 * 30
 Gln Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp
 CAG AAC TGG AGC CGG CCC TTC AAT GGG TCA GAA GAG GCA GAC
 40
 Arg Pro His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Thr Leu Ile
 AGG CCC CAC TAC AAC AAC TAC TAT TAT GCC ATG CTG CTC CTC CTC ATC
 50
 Phe Ile Ile Val Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser
 TTT ATC ATC GTC TTT GGC AAT-GTG CTG CTG GTG TGC ATG GCT GTA TCC
 60
 180

Arg	Glu	Lys	Ala	Leu	Gln	Thr	Thr	Thr	Asn	Tyr	Leu	Ile	Val	Ser	
GCA	GAG	AAG	GCT	TTG	CAG	ACC	ACC	ACC	AAC	TAC	TTG	ATA	GTC	AGC	
															70
Leu	Ala	Val	Ala	Asp	Leu	Val	Ala	Thr	Leu	Val	Met	Pro	Trp		90
CTT	GCT	GTG	GCT	GAT	CTT	CTG	GCC	ACA	CTG	GTA	ATG	CCG	TGG		
															270
Val	Val	Tyr	Leu	Glu	Val	Val	Gly	Glu	Trp	Lys	Phe	Ser	Arg	Ile	
GTT	GTC	TAC	CTG	GAG	GTG	GTG	GGT	GAG	TGG	AAA	TTC	AGC	AGG	ATT	
															100
His	Cys	Asp	Ile	Phe	Val	Thr	Leu	Asp	Val	Met	Met	Cys	Thr	Ala	
CAC	TGT	GAC	ATC	TTT	GTC	ACT	CTG	GAT	GTC	ATG	ATG	TGC	ACA	GCA	
															120
Ser	Ile	Leu	Asn	Leu	Cys	Ala	Ile	Ser	Ile	Asp	Arg	Tyr	Thr	Ala	
AGC	ATC	CTG	AAC	CTG	TGT	GCC	ATC	AGC	ATT	GAC	AGG	TAC	ACA	GCT	
															130
Val	Ala	Met	Pro	Met	Leu	Tyr	Asn	Thr	Arg	Tyr	Ser	Ser	Lys	Arg	
GTG	GCA	ATG	CCC	ATG	CTG	TAT	AAC	ACA	CGC	TAC	AGC	TCC	AAG	CGC	
															150
															450

FIG. 1B

Arg	Val	Thr	Val	Met	Ile	Ala	Ile	Val	Trp	Val	Leu	Ser	Phe	Thr
CGA	GTT	ACT	GTC	ATG	ATT	GCC	ATT	GTC	TGG	GTC	CTG	TCC	TTC	ACC
									160					
Ile	Ser	Cys	Pro	Leu	Leu	Phe	Gly	Leu	Asn	Asn	Thr	Asp	Gln	Asn
ATC	TCC	TGC	CCA	CTG	CTC	TTC	GGA	CTC	AAC	AAT	ACA	GAC	CAG	AAT
														540
Glu	Cys	Ile	Ile	Ala	Asn	Pro	Ala	Phe	Val	Val	Tyr	Ser	Ser	Ile
GAG	TGT	ATC	ATT	GCC	AAC	CCT	GCC	TTT	GTG	GTC	TAC	TCC	TCC	ATT
									190					
Val	Ser	Phe	Tyr	Val	Pro	Phe	Ile	Val	Thr	Leu	Leu	Val	Tyr	Ile
GTC	TCA	TTC	TAC	GTG	CCC	TTC	ATC	GTC	ACT	CTG	CTG	GTC	TAT	ATC
														630
Lys	Ile	Tyr	Ile	Val	Leu	Arg	Lys	Arg	Arg	Lys	Arg	Val	Asn	Thr
AAA	ATC	TAC	ATC	GTC	CTC	CGG	AAG	CGC	CGG	AAG	CGG	GTC	AAC	ACC
									220					
Lys	Arg	<u>Ser</u>	<u>Ser</u>	Arg	Ala	Phe	Arg	Ala	Asn	Leu	Lys	Thr	Pro	Leu
AAG	CGC	AGC	AGT	CGA	GCT	TTC	AGA	GCC	AAC	CTG	AAG	ACA	CCA	CTC
														720

FIG. 1C

[illegible]

990

Ser	Arg	Arg	Lys	Leu	Ser	Gln	Gln	Lys	Lys	Ala	Thr	Gln	340
AGC	CGC	AGA	AAG	CTC	TCC	CAG	CAG	AAG	AAG	GCC	ACT	CAG	
Met	Leu	Ala	Ile	Val	Leu	Gly	Val	Phe	Ile	Trp	Leu	Pro	360
ATG	CTT	GCC	ATT	GTT	CTC	GGT	GTG	TTC	ATC	TGC	CTG	CCC	
												1080	
Phe	Phe	Ile	Thr	His	Ile	Leu	Asn	Ile	Cys	Asp	Asn	Ile	370
TTC	TTC	ATC	ACG	CAC	ATC	CTG	AAT	ATA	TGT	GAT	TGC	ATC	
Pro	Pro	Val	Leu	Tyr	Ser	Ala	Phe	Thr	Trp	Gly	Tyr	Val	390
CCA	CCA	GTC	CTC	TAC	AGC	GCC	TTC	ACA	TGG	CTG	TAT	GTC	
												AAC	1170
Ser	Ala	Val	Asn	Pro	Ile	Ile	Tyr	Thr	Thr	Phe	Ile	Glu	400
AGT	GCC	GTC	AAC	CCC	ATC	ATC	TAC	ACC	ACC	TTC	AAC	GAG	
												TTC	
Arg	Lys	Ala	Phe	Met	Lys	Ile	Leu	His	Thr	TGC	TGAGTCTGCCCCCTTGCCTG	415	
CGC	AAG	GCC	TTC	ATG	AAG	ATC	TTG	CAC				1264	

FIG. 1E

CACAGCAGCTGCTTCCCACTCCCTGCCTATGCAGGCCAGACCTCATCCCTGCAAGCTG
TGGGCAGAAAGGCCCAGATGAACCTTGGCCCTTCTCTCGACCCCTGCAGCCCTGCAGTGTTA
1383
GCTTGGCTCGATGCCCCCTCTCTGCCCCACACACCCCTCATCTGCCAGGGTAGGGCCAGGG
AGACTGGTATCTTACCAGCTCTGGGGTTGGACCCATGGCTCAGGGCAGCTCACAGAGTGC
1502
CCCTCTCATATCCAGACCCCTGTCTCCTTGGCACCAAGATGCAGCGGCCCTTCCTTGACC
TTCCTCTTGGGCACAGAACTAGCTCAGTGGTCCAGCACACCCCTGATCGCTGGCTTGGCC
1621
TGGCCCTTGCTTGCCCTGTGCCGATCAGGTGGTGGGAGGGAGCGACACGTTCTTACTTT
ATAGGAACCACATAGGAAAGCAGGGAACACGCCCAAGTCTCCAGGCACATCAGTGTGAGG
1740
AGACACACATAAACACCAGGTAGCTCCATGGACCCCAAGAACTGAGGCTGAAAAATC
TGTTTTCCACTCCAACCTAGTGTGAGTCCCTACTTTTCATAGCCATGGGTATTACTATG
1859

FIG. 1F

TCCTACCTTGTTATAGTATCCCATGGGGTTTCTGTACCATTTGGGGGAAACAACACTCTA
 ATCCTCAAGGGCCCAAGAGAACTCTGTAGGAGAAAAATAGGCTGATCTCCCTCTACTCT
 CCAATCCACTCCACCACCTTCTTGATATACCTTGGATGTATCCATTCCTCACAGCAAATG 1978
 CTGGCCAGTCAGGCCTTGGACCAGTGTGGAGTTGAAGCTGGATGTGGTAACTTGGGGCT
 CTTGGGGCTGGGGGGTGTAAACATCGTCTCTCTTCCATATCTCTTCCCTTCCCAGTG 2097
 CCTCTGCCCTTAGAAGAGGCTGTGGATGGGGTGCTGGGACTGCTGATACCATTTGGGCCTGG
 CCCTGAATGAGGAGGGGAAGCTGCAGTTTGGAGGTTCTGGGATCCAACTCTGTAAACAT 2216
 CACTATACCTGTACCAAACTAATAAACCTTGACAAGAGTCAAAAA 2317

FIG. 1G

D₆
β₆
α₆
G-21
M₁
SK

I
MD... PL... NISWYDDLLERQNSRPFNGSEKADRPYNYAMITLL. IFIIVFGNVLVCMVAVSREKALQTHINY
MGP... P... QNDSDFLLTNGSHV... PDHVDTEERDEAVVVGMAIMSVIVLAVFGNVLVITAIKAFERLOTVINY
MGSLLQ. POA. QNASWNGTEAPG... GGARATPYSLQVT... LTLVCLAGLL. MLLTVFGNVLVITAVFTSRATKAPQNL
MDVLS. PQQ. QNNTSPPAPFE... TGCNTTGISDVTVSQV. ITSLLIGTL. IFCAVTCNAGVAVAIALERSLQNVANY
MNTSAPPVSPNITVLAP... GKGWQVA... FIGITTL. SLATVTCNLTIIISFKVNTETKTVNY
MGACV. VMTDINIS. SGLDSNATGITAFSMPGWQLALWTAAYLAL. VLVAVMGNATVWIIILAHQRMRTVINY

D₆
β₆
α₆
G-21
M₁
SK

II
LIVSLAMADIVATLVMPWVVYLEVQMFPSRIHCDIFVILDVMMCTASILNLCASIQRYTAVAMPMTIMTRYSSKPR
FIDSACADIVMGIAVMPFGASHIIMKMNFGNFWCEFWTSIQVLCVTASTETLCVIAVQRYIAITSEFKYQSLTKNKA
FIVSLASADILVATLVMPFSLANEVQMYMECKTWCEIYALDVLCTSSIVHLCAISIQRYWSTQAIETNLKRTPRRI
LIGSLAVTIDIMSVLVITHEMAALYQMLNNWTLQVTCDFIALDVLCTSSILHLCAIAIQRYWSTQAIETNLKRTPRRI
FLLSLACADILIIIGFSNLYTTLIMQIMALGTIACDLWLALDYVASNA SUMNLLIISFQRYFSVTRPLSYRAKTRPRRA
FIVNLALADICMAAFNAFVYASHNIMYEGRACFCYQNLFPITAMFVSIYSMTAIAAQRYMAIVRPFQRLSAPGTR.

D₆
β₆
α₆
G-21
M₁
SK

V
VTMTAIVWVISETISC. PLLFGLNNTD... QNECIANPAFVVYSSIMSFYVPLVILLVYIKIVILVRKRKRVTNR--(111)
RMV. IILMVIVSGLTSFPIQMHWRATH... QKAIDCYHRETCCDFFTNQAYATWSSIVSFYVPLVILLVYIKIVILVRKRKRVTNR--(111)
KAI. IITVWVISAVIDSFPLISIEKKGG... GGPQPAEPRCEINDQKVVITSSCIGSFAPOHIMILVWVRIYQIAKRTRVP--(137)
ALT. SLT. MLIGTLISIPMLGWRTPEDR... SDPDACTISKDMGYTIVSTFGAFYIPILMLVLYGRIFRAARFIPIT--(110)
ALM. IGLAMLVSEVLWA. PAILFWQYLVE... RTVLACQCYIQFLSQPIITFGTAMAAFYLPVTMCTIYWRIYRETNAREL--(137)
.AV. IAGTLLVALALAF. PQCFYSTITDEGATKCVVAVPEDSGGKMLLLYHLIVIALIYE. LPVWVAVSVIGLTLWRSVPG--(12)--

D₆
β₆
α₆
G-21
M₁
SK

VII
-KEKKAITQMTAIVIMFTHCWLPPFFITHIINIHCOCN... IPVLYSAFTWLGYNVSA... VNPITYITFNIETFRNAPMKILHC
-KEKKAITQMTAIVIMFTHCWLPPFFITHIINIHCOCN... IPVLYSAFTWLGYNVSA... VNPITYITFNIETFRNAPMKILHC
-REKRTFVIAVIMFTHCWLPPFFITHIINIHCOCN... IPVLYSAFTWLGYNVSA... VNPITYITFNIETFRNAPMKILHC
-REKRTVKTQIMGIFILCWIPFFITHIINIHCOCN... IPVLYSAFTWLGYNVSA... VNPITYITFNIETFRNAPMKILHC
-KEKKAARTSAILLAFIVIMFTHCWLPPFFITHIINIHCOCN... IPVLYSAFTWLGYNVSA... VNPITYITFNIETFRNAPMKILHC
-AKKYFVKTMVIMFTHCWLPPFFITHIINIHCOCN... IPVLYSAFTWLGYNVSA... VNPITYITFNIETFRNAPMKILHC

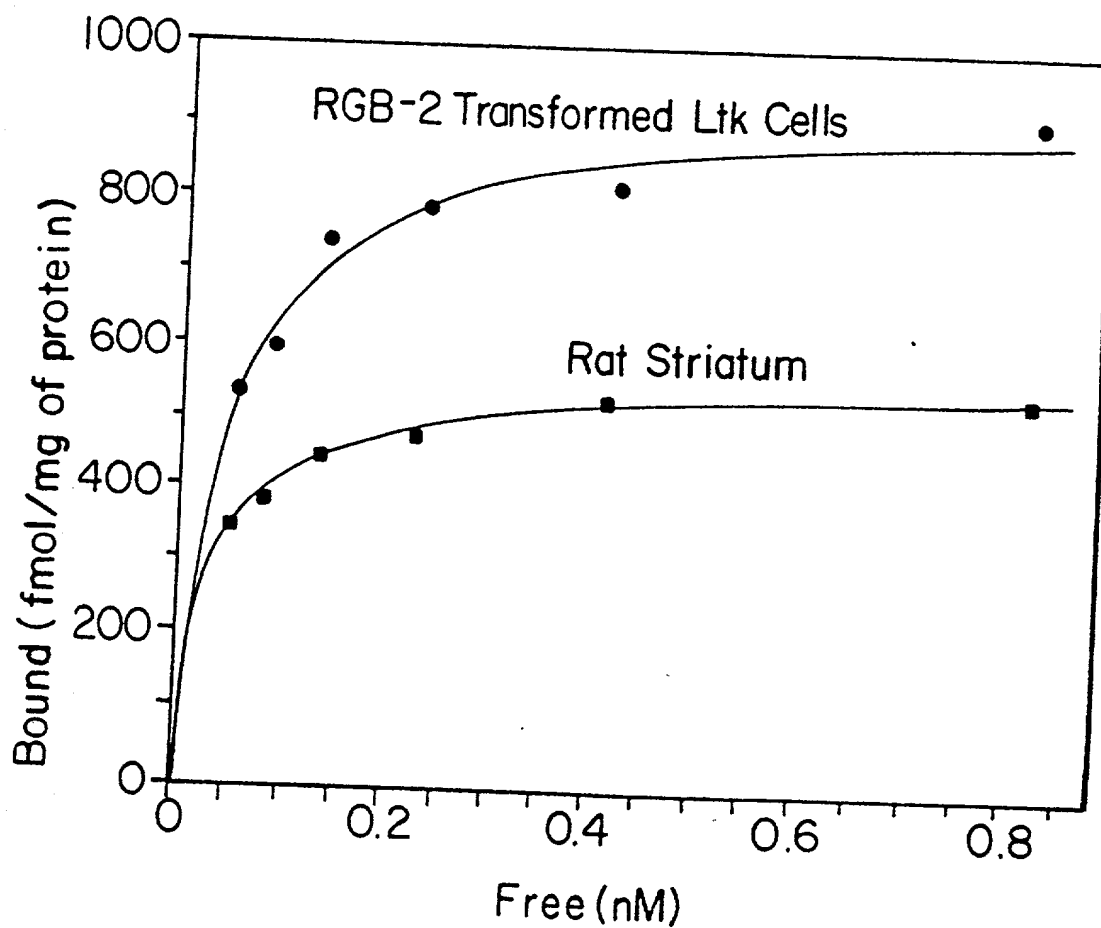


FIG.4A-1

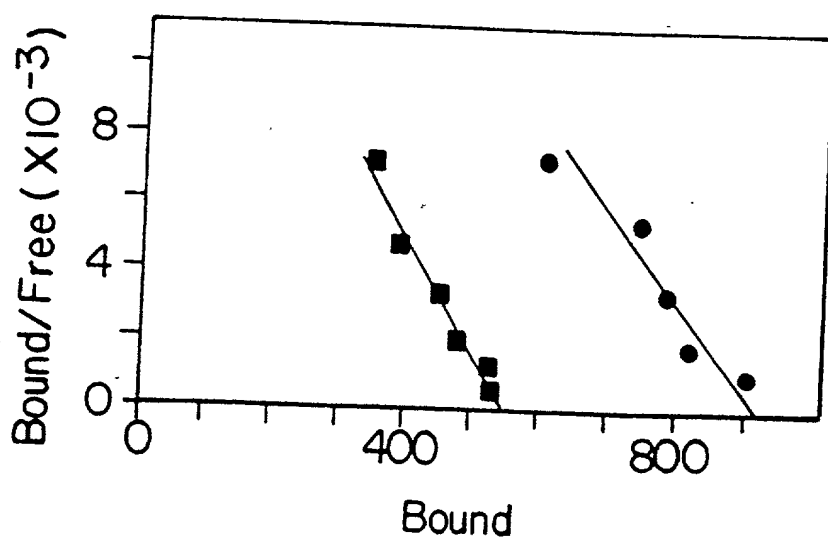
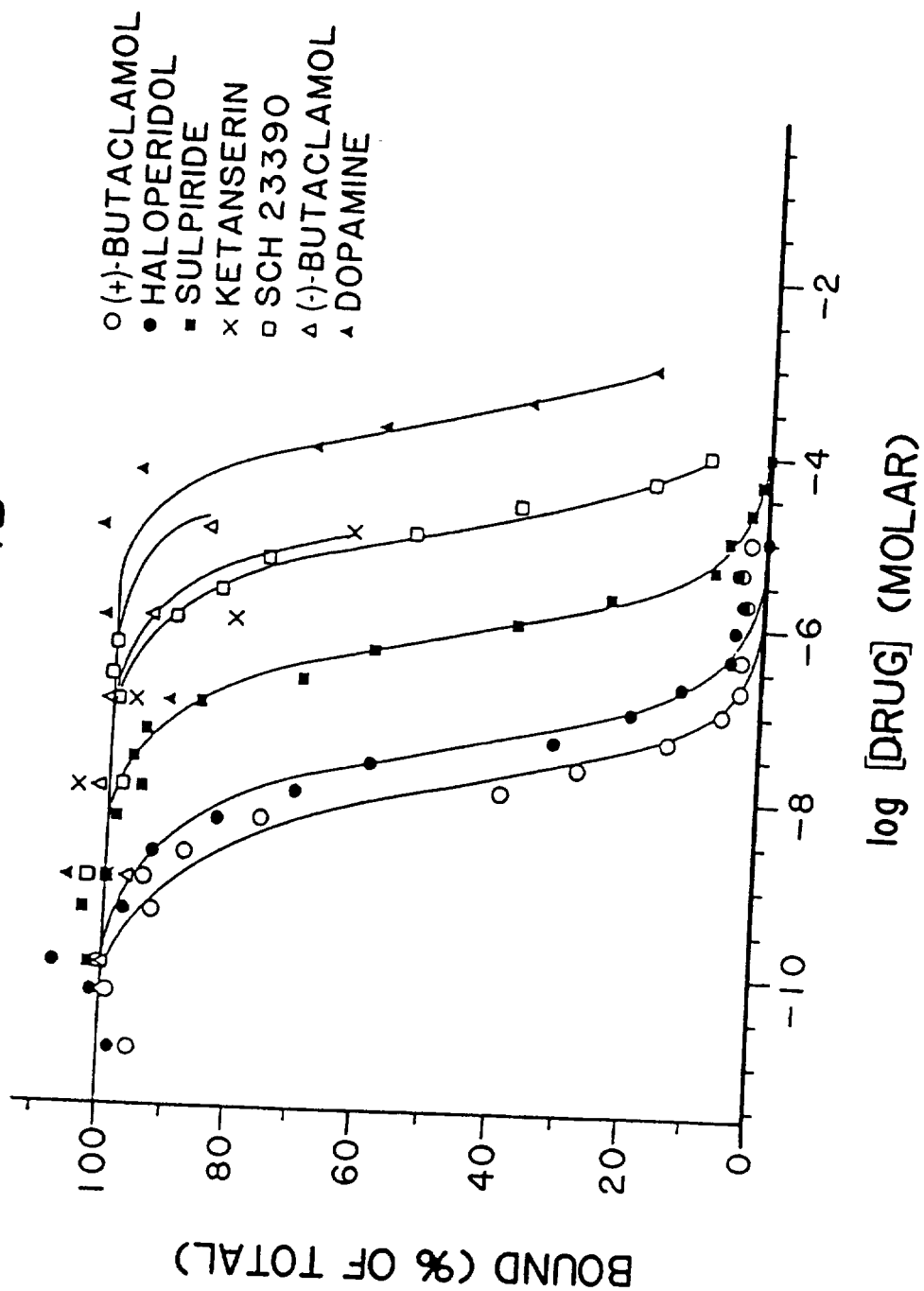


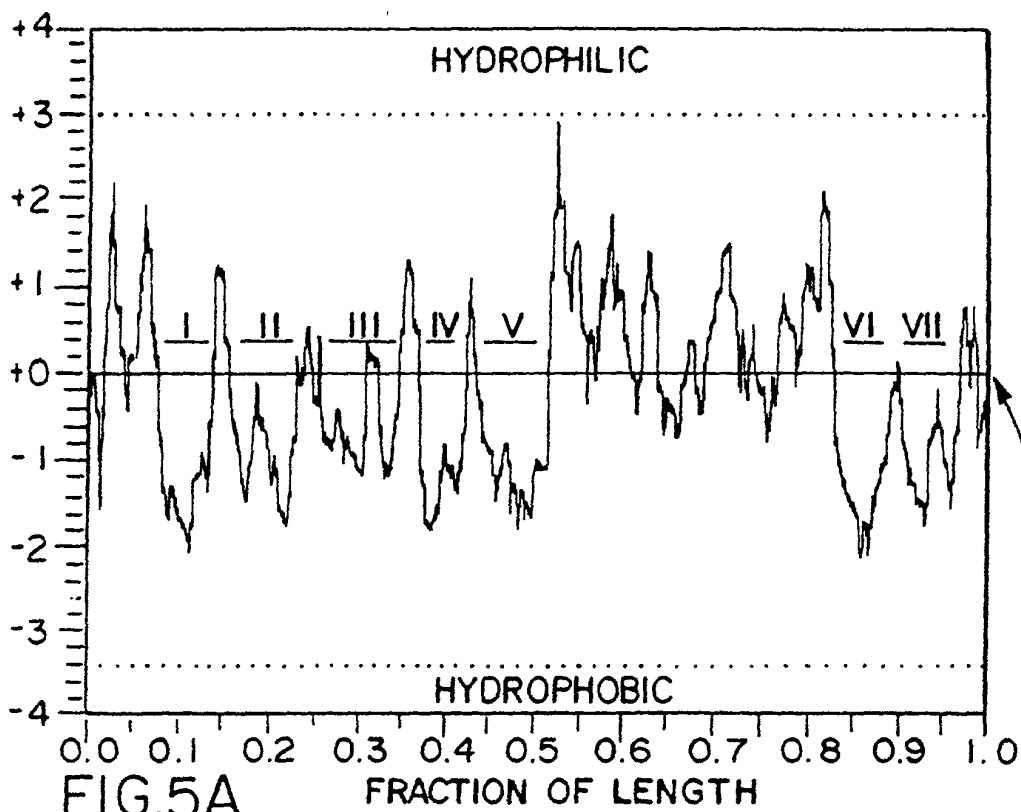
FIG.4A-2

FIG. 4B



DRUG		Ki (nM)	
		Transformed Ltk-Cells	Rat Striatum
RGB-2			
(+)-Butaclamol	0.83	1.0	
(-)-Butaclamol	>1,000	>1,000	
Haloperidol	3.0	5.3	
Dopamine + GTP	17,000	6,300	
Sulpiride	80	67	(87%)
high affinity	---	>10,000	(13%)
low affinity			
SCH 23390	---	35	(16%)
high affinity	---	780	(84%)
low affinity	1,000		
Ketanserin	---	27	(25%)
high affinity	---	>1,000	(75%)
low affinity	>1,000		

FIG. 4C



RGB-2

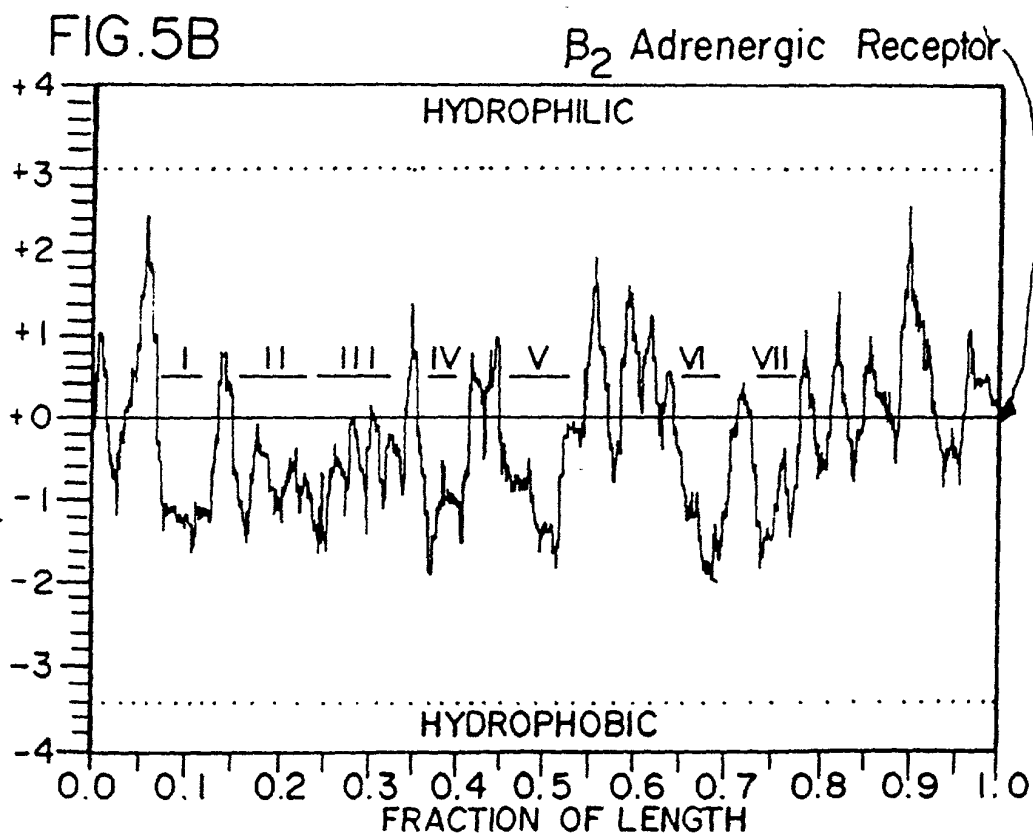
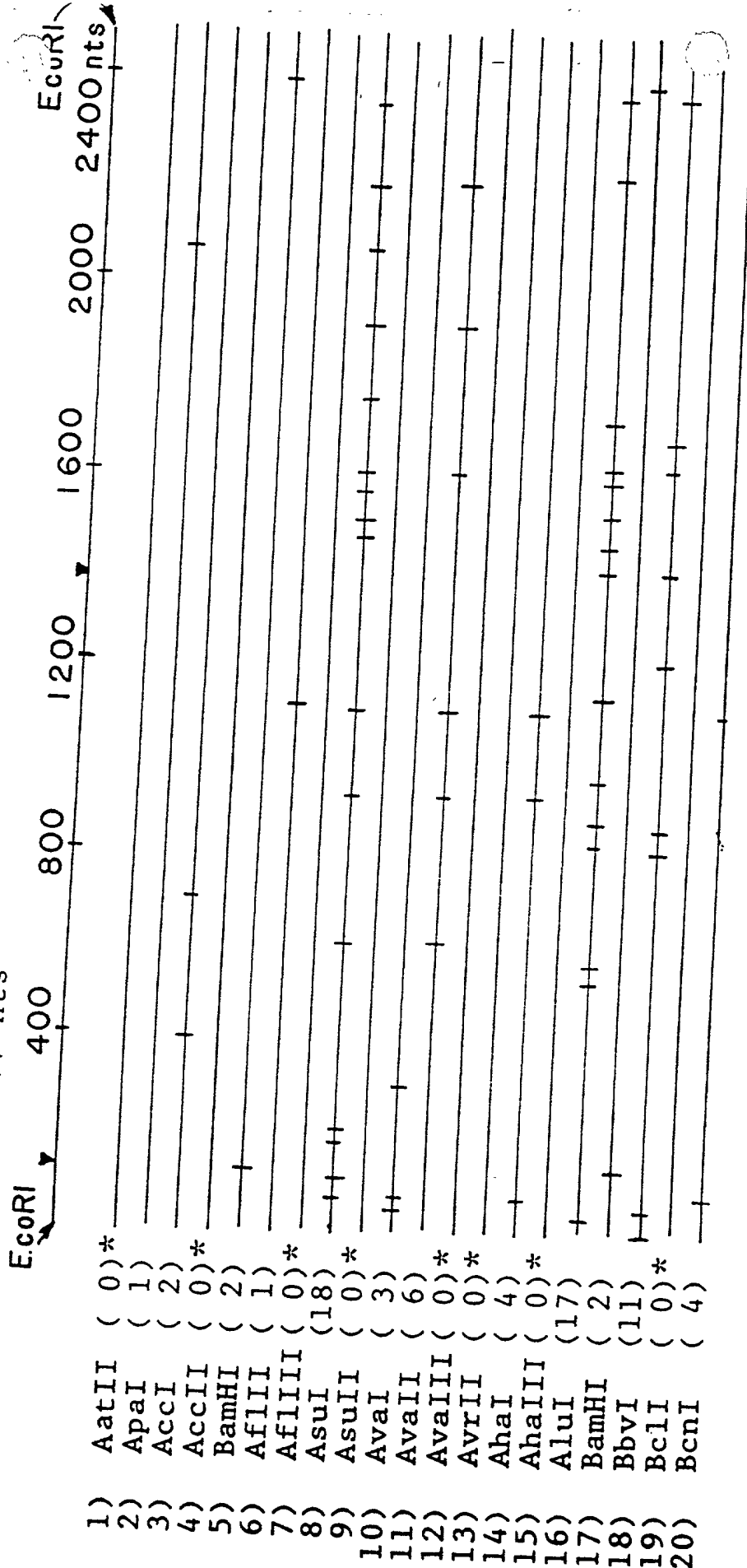


FIG. 6A

Length of DNA: 2477 nts



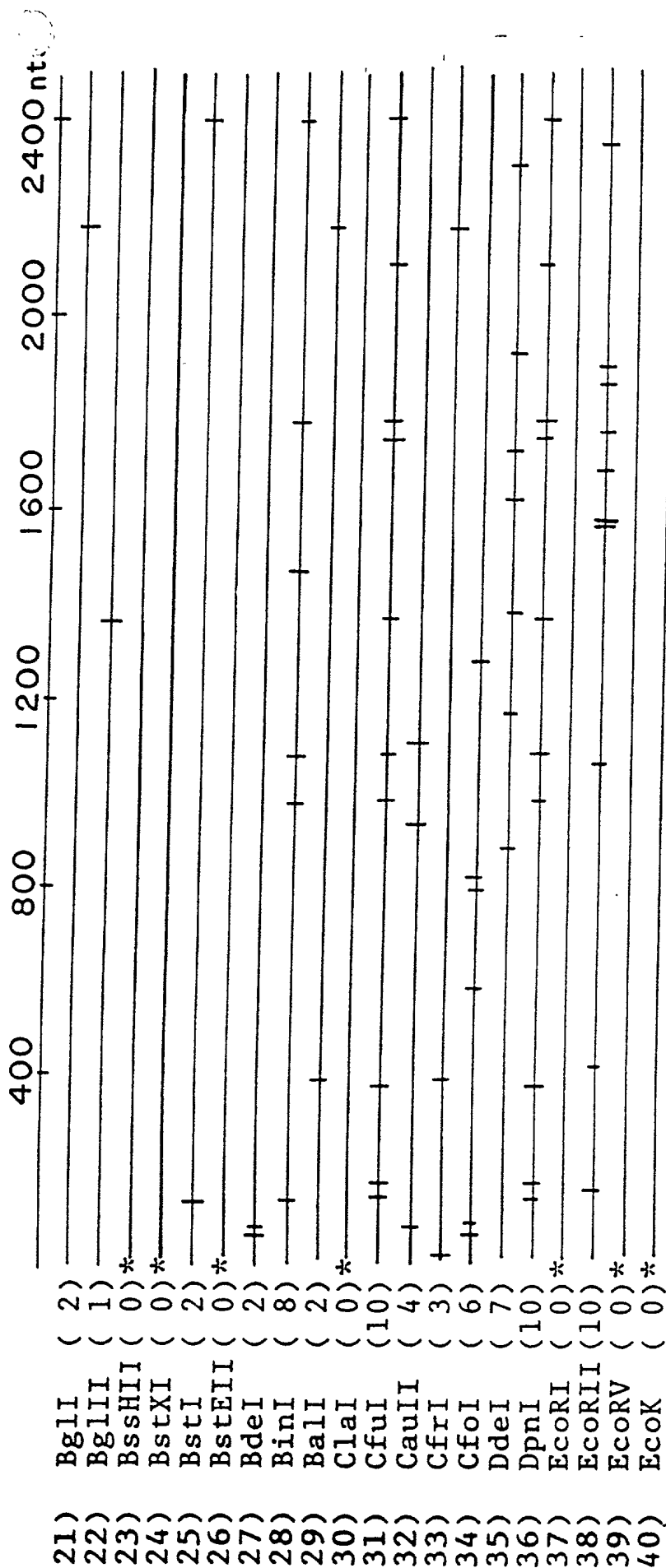


FIG. 6B

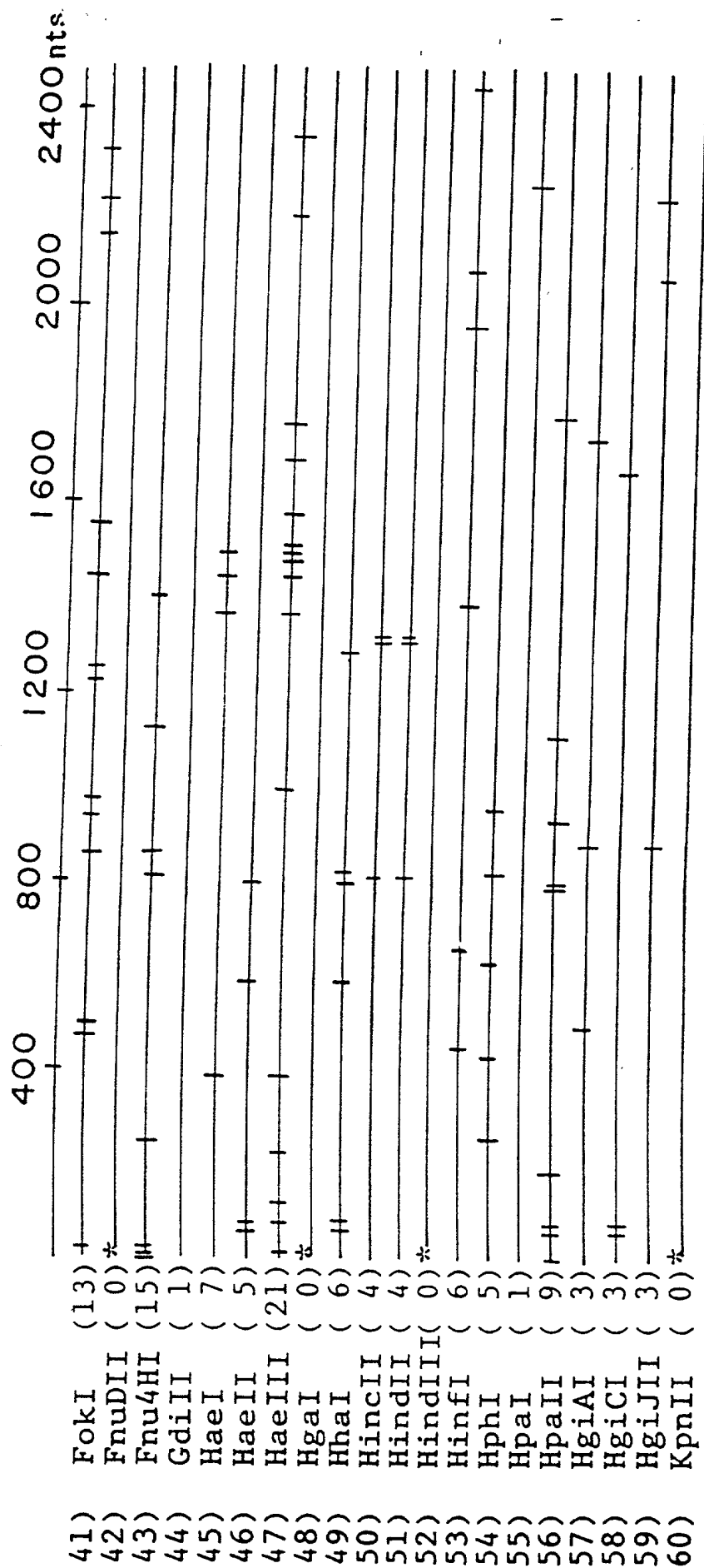


FIG. 6C

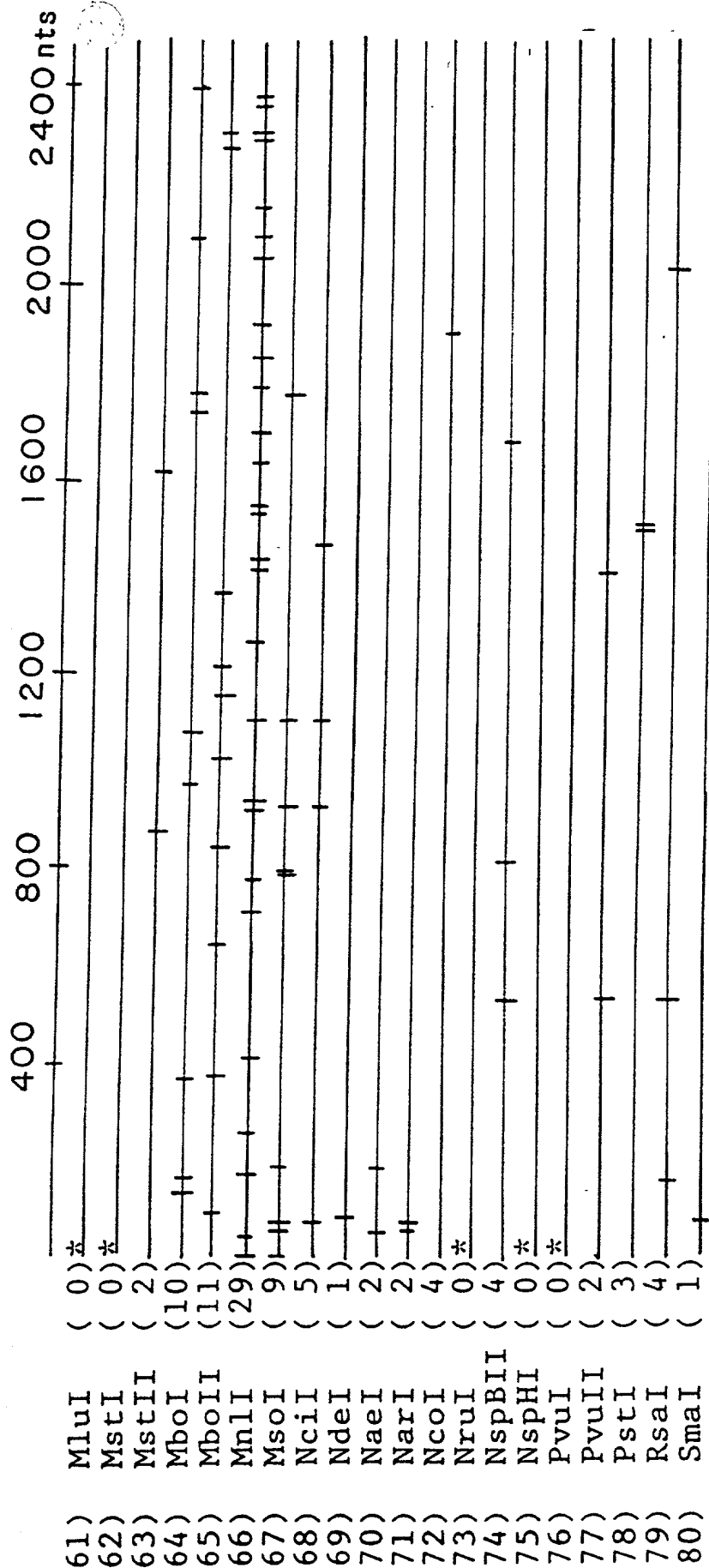


FIG. 6D

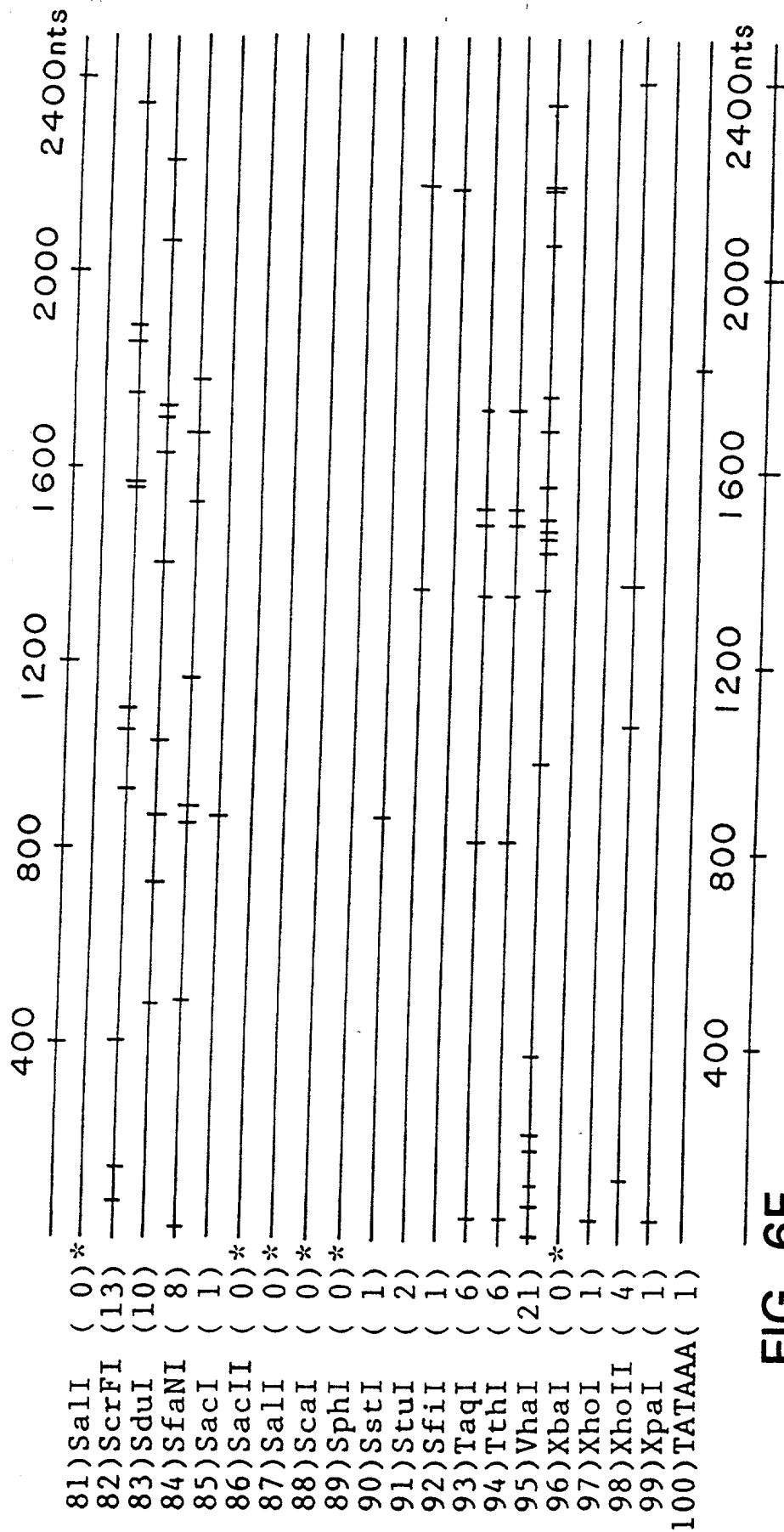


FIG. 6E

FIG. 7A

3' GTC GGG TGG GCT CTC CTC GGC CAT GTC GGG GTA GGG TGG GTC GGT GGT GGT CGA 5' 54
 5' CAG CCC ACC CGA GAG GAC CCG GTA CAG CCC CAT CCC ACC CAG CCA CCA CCA GCT 3' 54
 Gln Pro Thr Arg Glu Asp Pro Val Gln Pro His Pro Thr Gln Pro Pro Pro Ala
 Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln Leu
 Ala His Pro Arg Gly Pro Gly Thr Ala Pro Ser His Pro Ala Thr Thr Ser

81
 CTG AGA GGG GCT GGT CAG GGT GGT ACC AGA GGT GTC GTG AGG GCT GTC GGT GGT 108
 GAC TCT CCC CGA CCC GTC CCA CCA TGG TCT CCA CAG CAC TCC CGA CAG CCC CGC
 Asp Ser Pro Arg Pro Val Pro Pro Trp Ser Pro Gln His Ser Arg Gln Pro Arg
 Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp Ser Pro Ala
 Leu Ser Pro Thr Arg Pro Thr MET Val Ser Thr Ala Leu Pro Thr Ala Pro Pro

135
 GTT TGG TCT CTT CTT ACC CGT ACC GGT TTC CTG GTG GGG TTC CTA ACG GTT CTA 162
 CAA ACC AGA GAA GAA TGG GCA TGC CAA AAG GAC CAC CCC AAG GAT TGC CAA GAT
 Gln Thr Arg Glu Glu Trp Ala Cys Gln Lys Asp His Pro Lys Asp Cys Gln Asp
 Lys Pro Glu Lys Asn Gly His Ala Lys Arg Thr Thr Pro Arg Ile Ala Lys Ile
 Asn Gln Arg Arg MET Gly MET Pro Lys Gly Pro Pro Gln Gly Leu Pro Arg Ser

189
 GAA ACT CTA GGT CTG CTG GTA CCG GTT ACC GTT TTG GGC CTG GAG GGA GTT CTG GTA 216
 CTT TGA GAT CCA GAC CAT GCC CAA TGG CAA AAC CCG GAC CTC CCT CAA GAC CAT
 Leu . Asp Pro Asp His Ala Gln Trp Gln Asn Pro Asp Leu Pro Gln Asp His
 Phe Glu Ile Gln Thr MET Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr MET

FIG. 7B

CTC GGC ATC CTT C6A G55 GGT CGT CTT CCT CTT TCG GTG AGT CTA CGA GCG 270
GAG CCG TAG GAA G3T C44 CCA GCA GAA GGA GAA AGC CAC TCA GAT GCT CGC
Glu Pro . Glu C TT Pro Ala Glu Gly Glu Ser His Ser Asp Ala Arg
Ser Arg Arg Lys Leu Phe Gln Gln Lys Glu Lys Lys Ala Thr Gln MET Leu Ala
Ala Val Gly Ser Ser Arg Arg Arg Lys Pro Leu Arg Cys Ser Pro

243
GTA 5CA AGA GCC GCA CAA GTA GTA GAC GAC CGG GAA GAA GTA GTG TGT GTA 324
CAT 4GT TCT CCG CGT GTT CAT CAT CTG CTG GCT GCC CTT CTT CAT CAC ACA CAT
His T Ser Arg Arg Val His His Leu Ala Ala Leu Leu His His Thr His
ILE Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile
le Phe Ser Ala Cys Ser Ser Ser Ala Gly Cys Pro Ser Ser His Thr Ser

297
GGA CTT GTA TGT GAC ACT GAC GAC GGT GAC GGT CGG ACA GGA CAT GTC GCG GAA GTG 378
CCT GAA CAT ACA CTG TGA CTG CAA CAT CCC GCC TGT CCT GTA CAG CGC CTT CAC
Pro Glu His Thr Leu . Leu Gln His Pro Ala Cys Pro Val Gln Arg Leu His
Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr
. Thr Tyr Thr Val Thr Ala Thr Ser Arg Leu Ser Cys Thr Ala Pro Ser Arg

351
CAC CGA CCC GAT ACA GTT GTC GCG GCA CTT GGG GTA GTA GAT GTG GTG GAA GTT 432
GTG GCT GGG CTA TGT CAA CAG CGC CGT GAA CCC CAT CAT CTA CAC CAC CTT CAA
Val Ala Gly Leu Cys Gln Gln Arg Arg Glu Pro His His Leu His His Leu Gln
Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn
Gly Trp Ala MET Ser Thr Ala Pro . Thr Pro Ser Ser Thr Pro Pro Ser Thr

405

459
 GTA ACT CAA GGC GTT CCG GAA GGA CTT CTA GGA GGT GAC GAC TGA GAC GAC GAC 486
 CAT TGA GTT CCG CAA GGC CTT CCT GAA GAT CCT CCA CTG CTG ACT CTG CTG CTG GGA
 His . Val Pro Gln Gly Leu Pro Gln Asp Pro Leu His Cys STOPLeu Cys Cys Leu
 Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys STOPLeu Cys Cys Leu
 Leu Ser Ser Ala Arg Pro Ser . Arg Ser Ser Thr Ala Asp Ser Ala Ala Cys

513
 CGG CGT GTC GTC GGA CGA AGG GTG CAG GGA CGG GTC ACG GCC GGT CGG AGT GGT 540
 GCC GCA CAG CAG CCT GCT TCC CAC CTC CCT GGC CAG TGC CGG CCA GCC TCA CCC
 Ala Ala Gln Gln Pro Ala Ser His Leu Pro Ala Gln Cys Arg Pro Ala Ser Pro
 Pro His Ser Ser Leu Leu Pro Thr Ser Leu Pro Ser Ala Gly Gln Pro His Pro
 Arg Thr Ala Ala Cys Phe Pro Pro Cys Pro Val Pro Ala Ser Leu Thr Leu

567
 AAC GCT TGG CAC TCG TCC TTC CCG ACC CAC CTA GCC GGA GAA GAT CGG GGC 594
 TTG CGA ACC GTG AGC AGG AAG GCC TGG GTG GAT CGG CCT CCT CTT CTA GCC CCG
 Leu Arg Thr Val Ser Arg Lys Ala Trp Val Asp Arg Pro Pro Leu Leu Ala Pro
 Cys Glu Pro . Ala Gly Arg Pro Gly Trp Ile Gly Leu Leu Phe . Pro Arg
 Ala Asn Arg Glu Gln Glu Gly Leu Gly Ser Ala Ser Ser Ser Ser Pro Gly

FIG. 7C

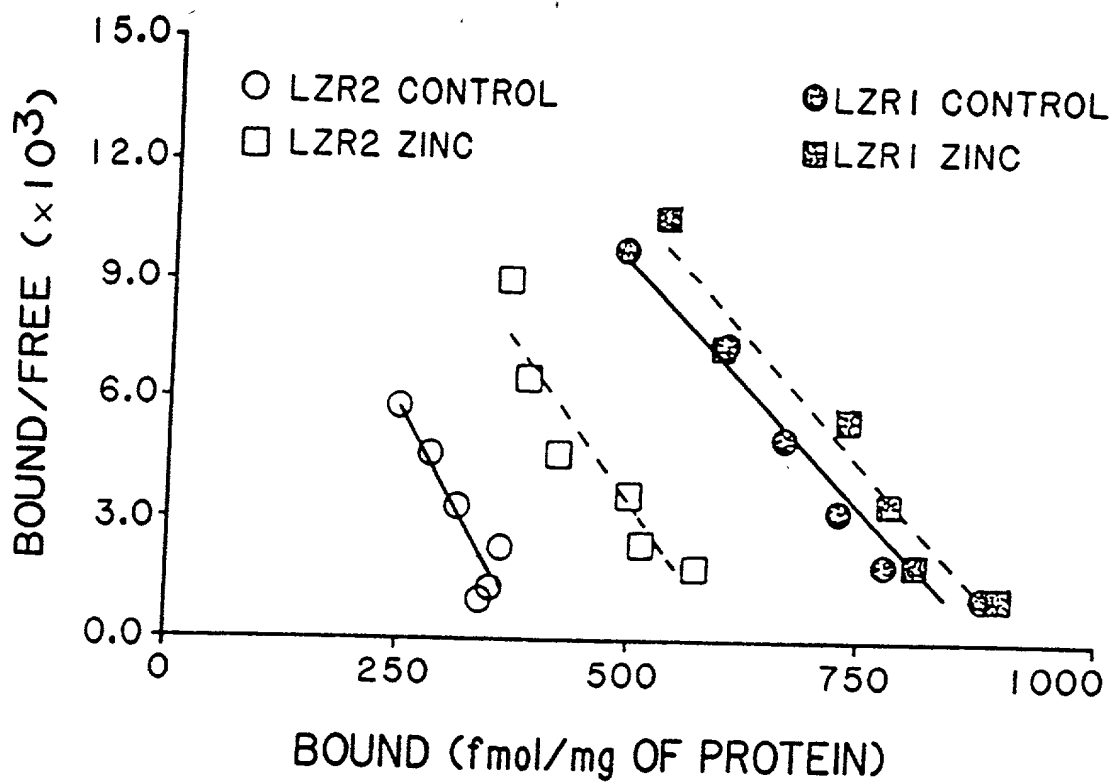


FIG. 8

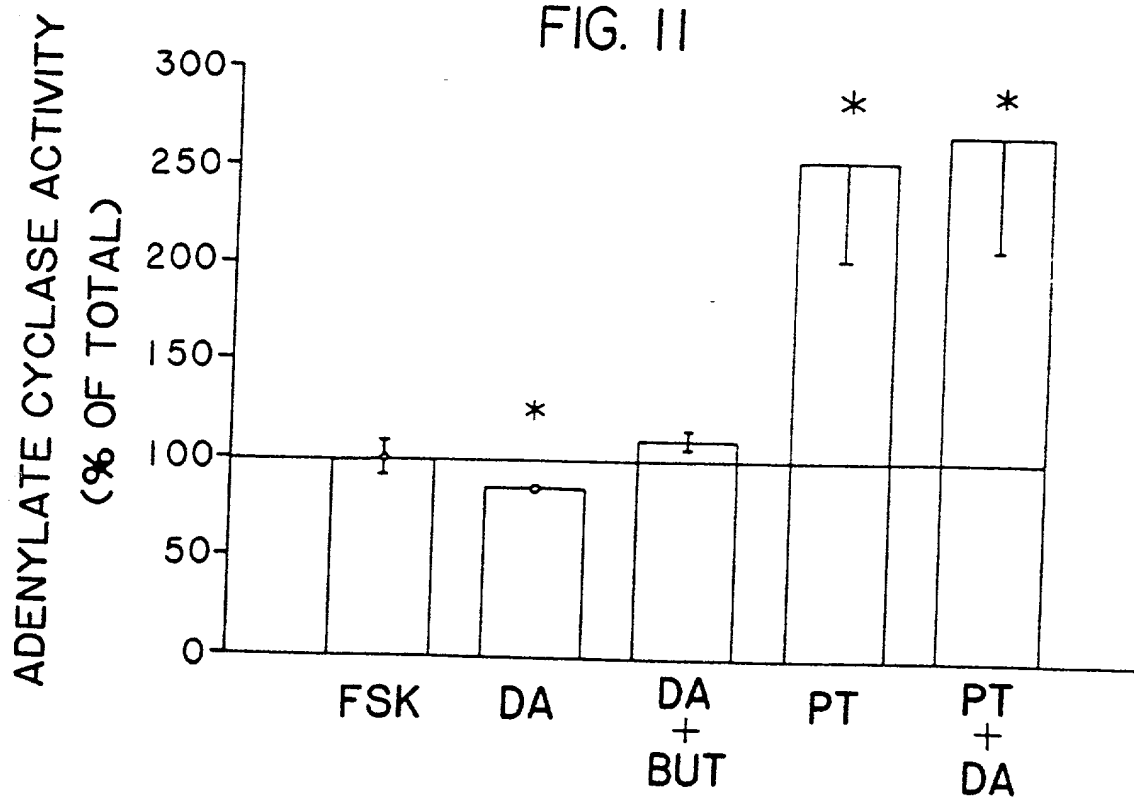


FIG. 9A

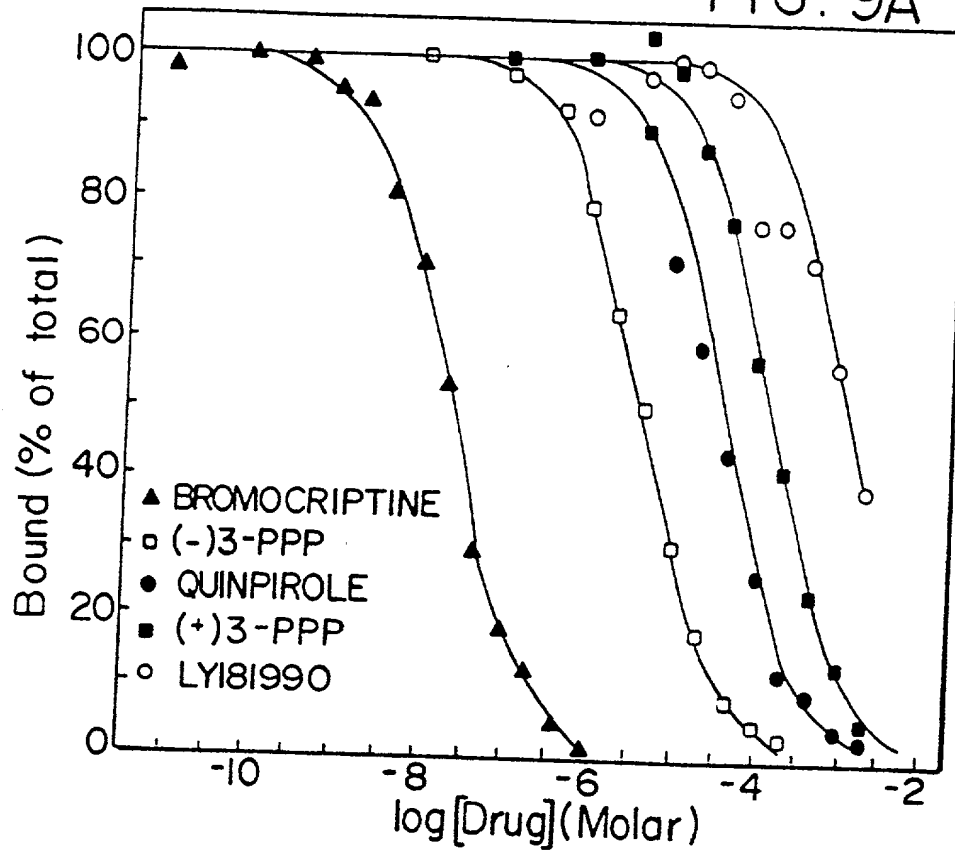
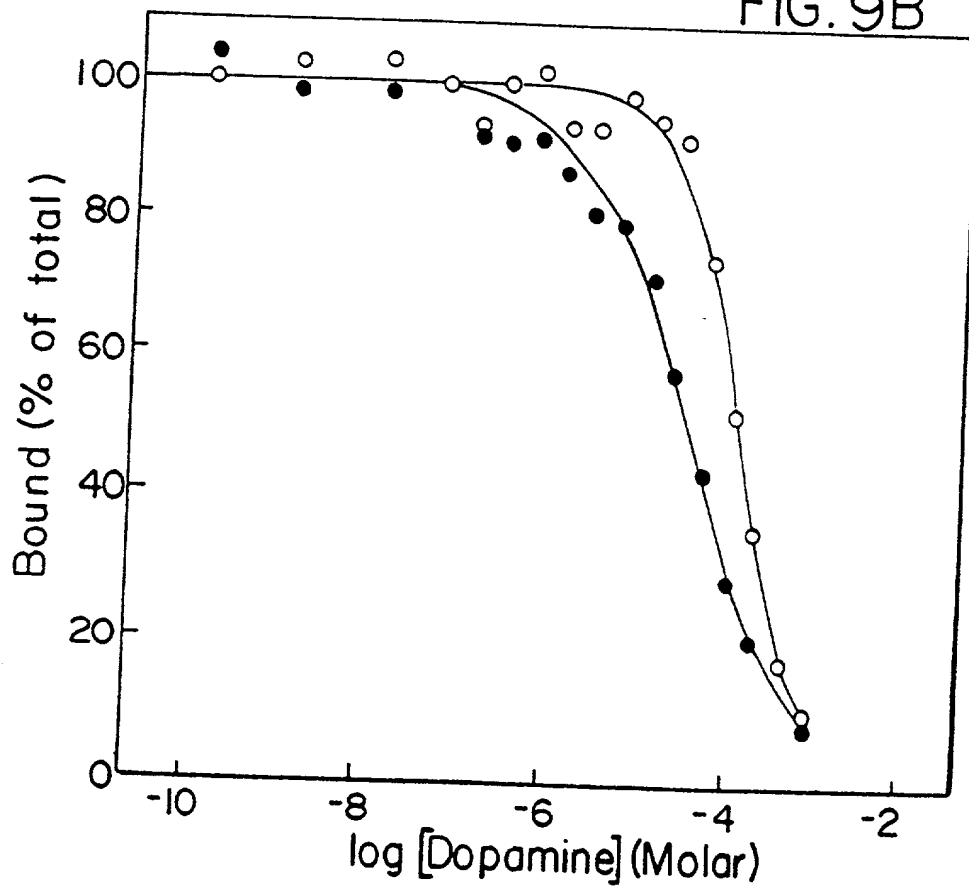


FIG. 9B



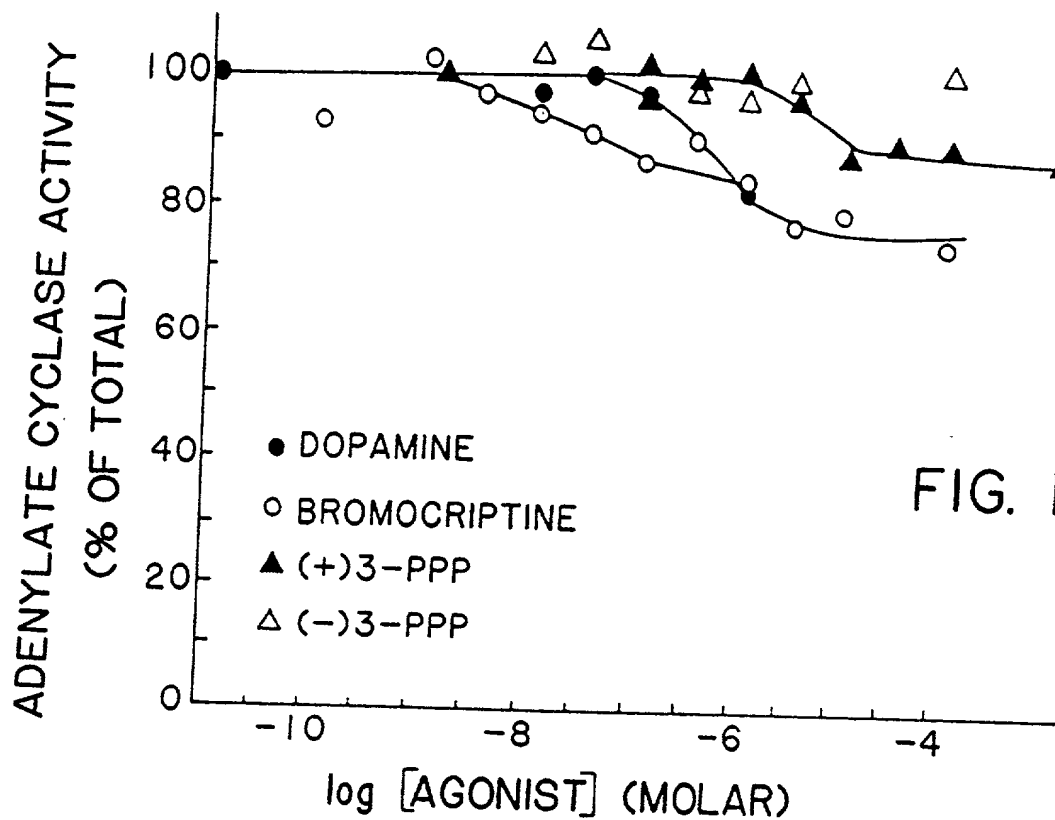


FIG. 10A

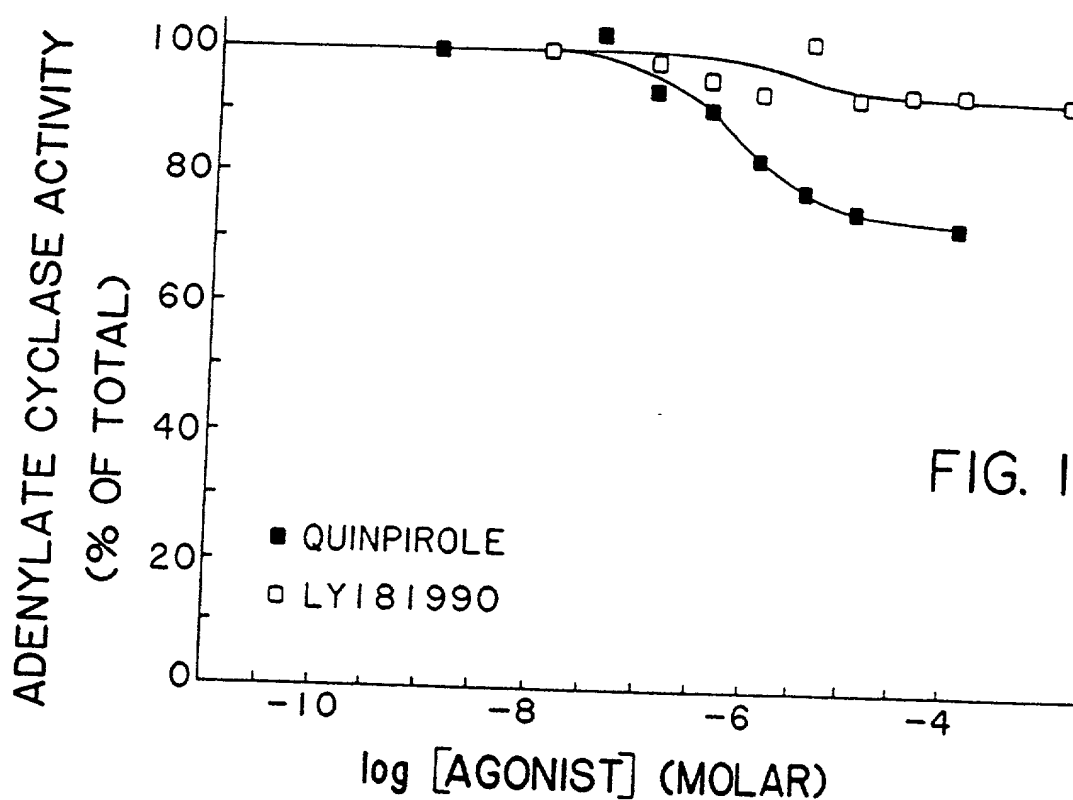


FIG. 10B

CONTROL

		+P.T.			
BASAL	FSK	FSK+DA	BASAL	FSK	FSK+DA
2.1	22.6	14.3	1.7	26.7	23.1
0.2	2.2	2.1	0.4	2.0	0.5
—	—	41%	—	—	14%

\bar{X}
S.E.

FIG. 12A

INH

CONTROL

				+P.I.			
BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
0.60	2.41	0.32	0.84	0.61	2.68	0.55	2.56
0.02	0.31	0.02	0.13	0.09	0.08	0.03	0.25
—	—	53%	71%	—	—	10%	3%

\bar{X}
S.E.

FIG. 12B

INH

CONTROL

				+P.I.			
BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
0.78	5.1	0.25	0.76	0.64	5.29	0.66	4.76
0.04	0.4	0.03	0.01	0.01	0.44	0.03	0.16
—	—	68%	88%	—	—	0%	12%

\bar{X}
S.E.

FIG. 12C

INH

FIG. 13B-1

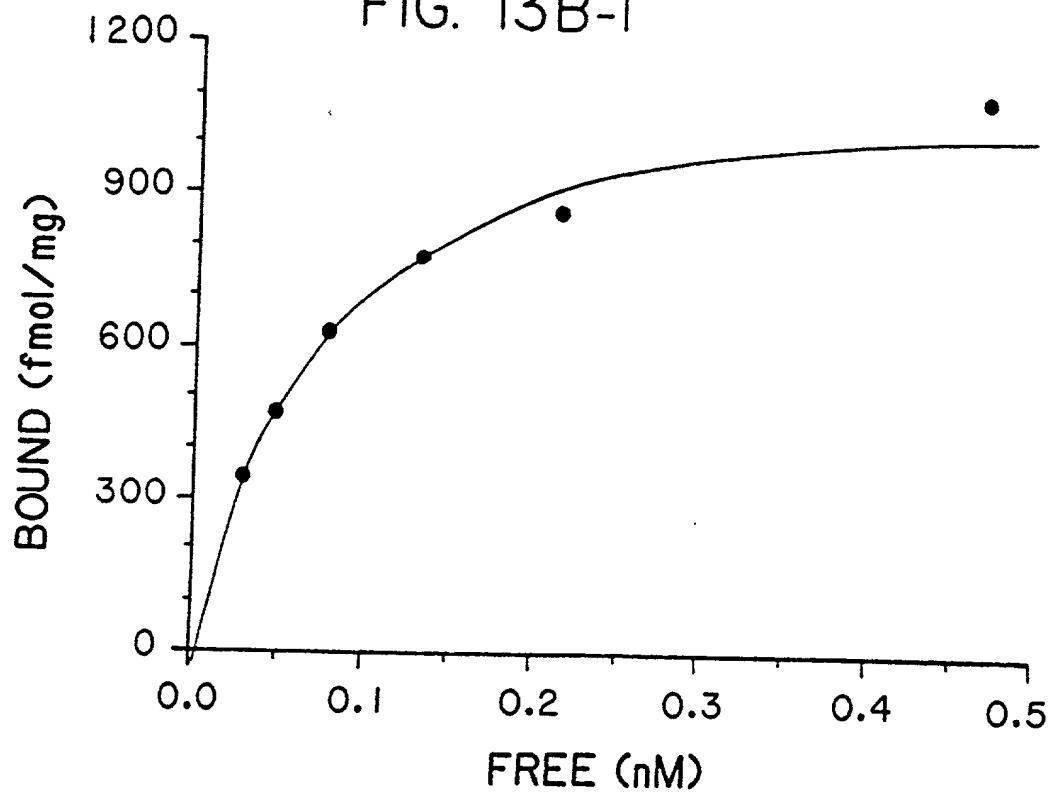


FIG. 13B-2

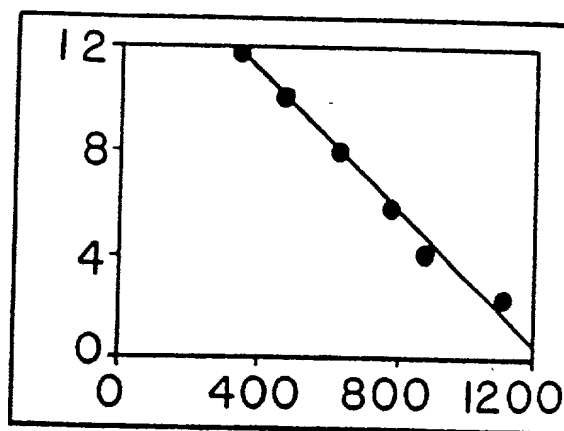


FIG. 13C

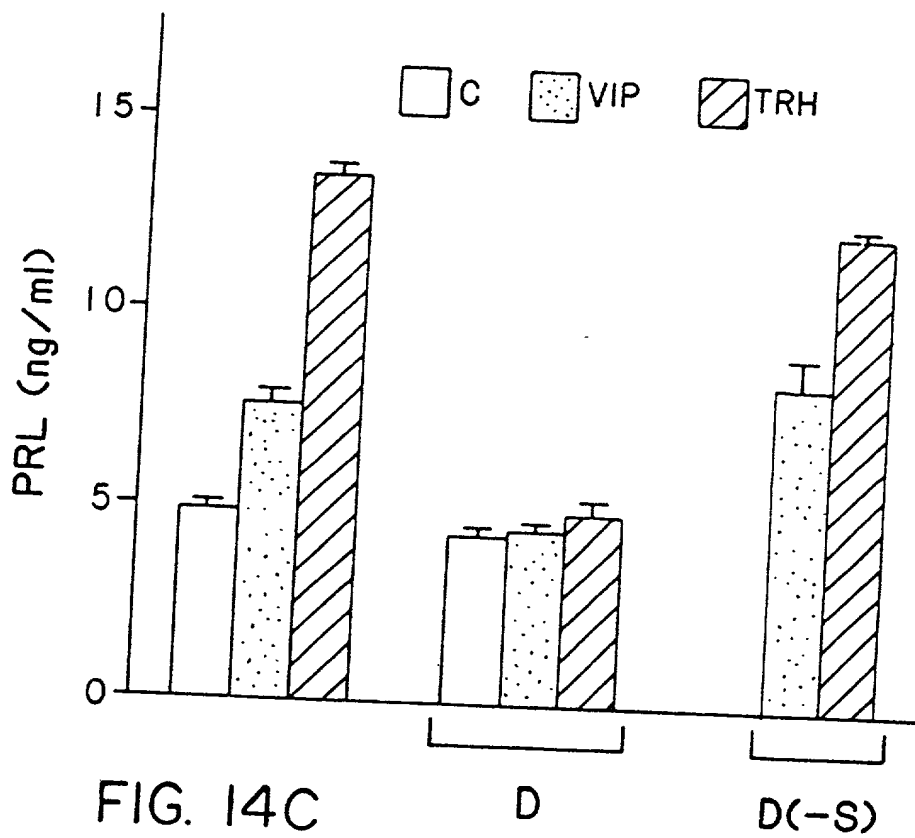
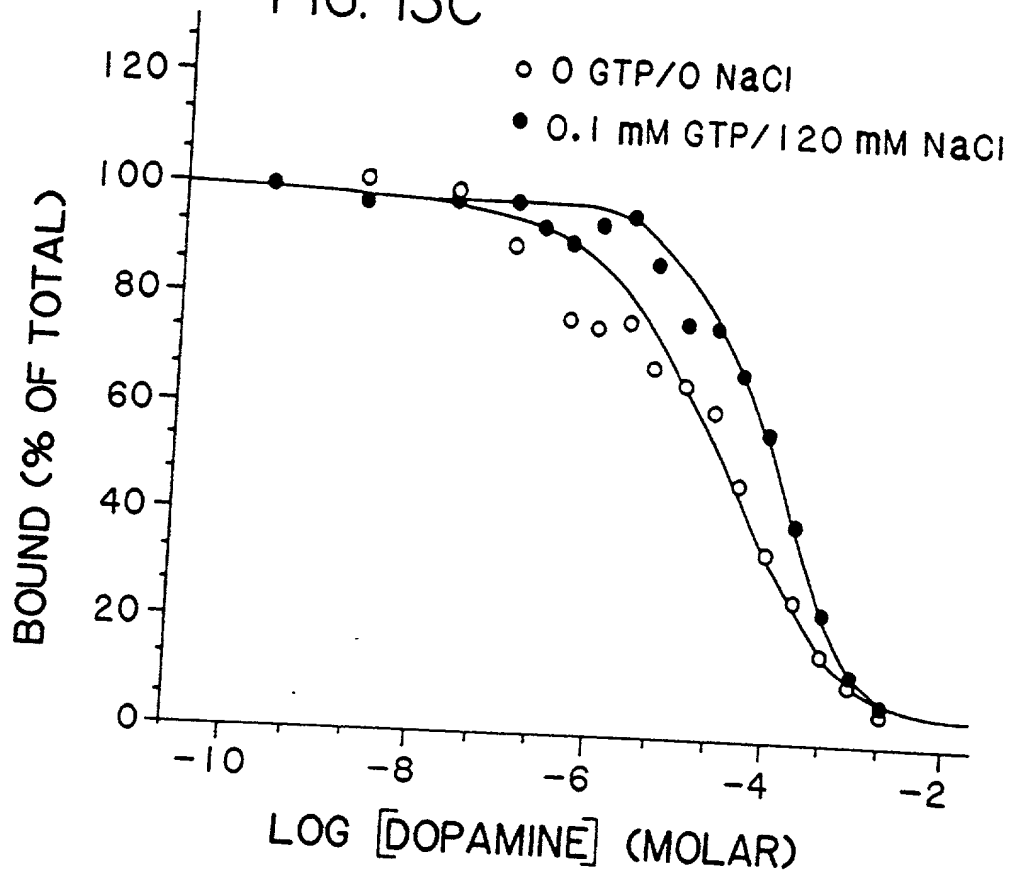


FIG.14A

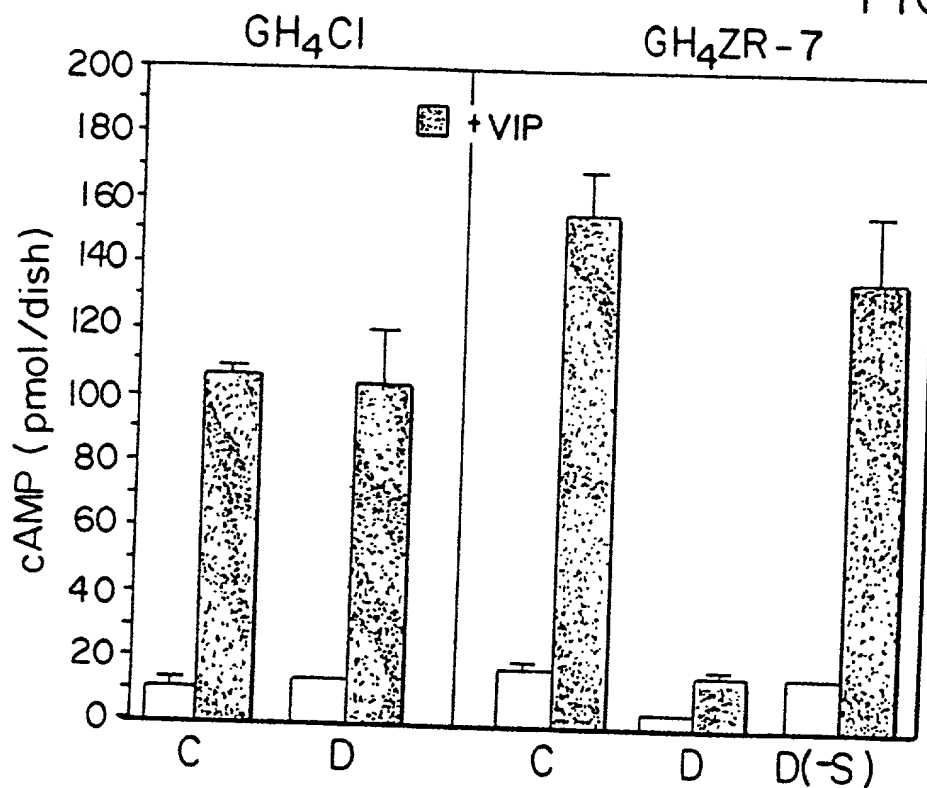
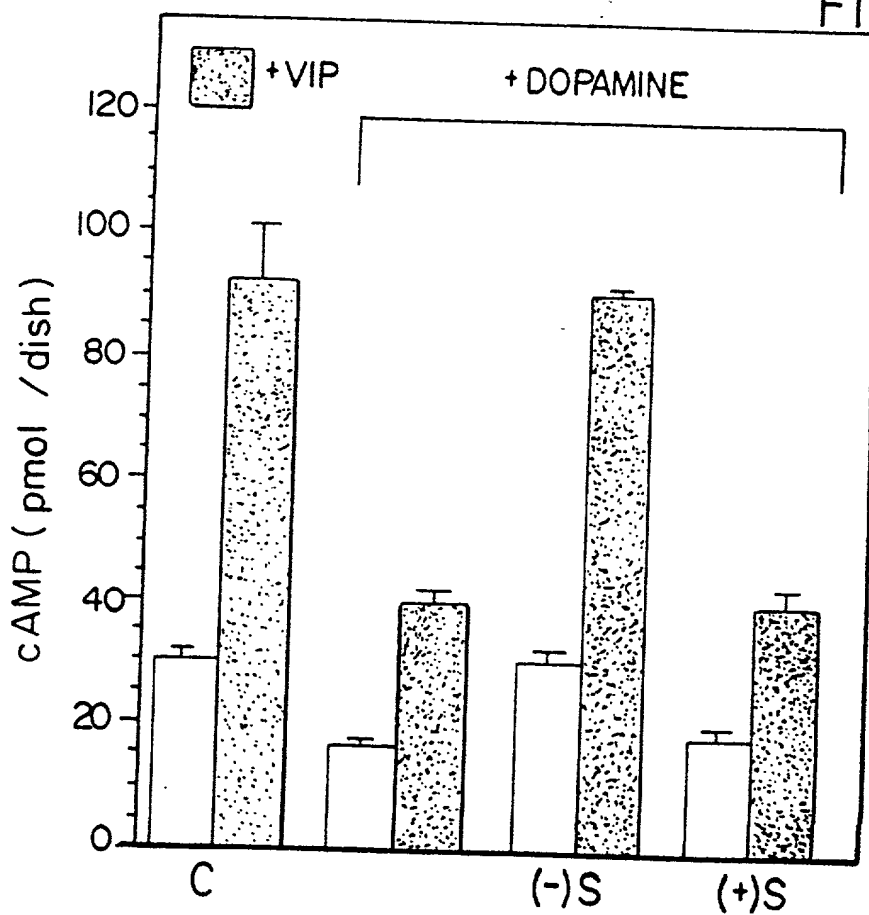
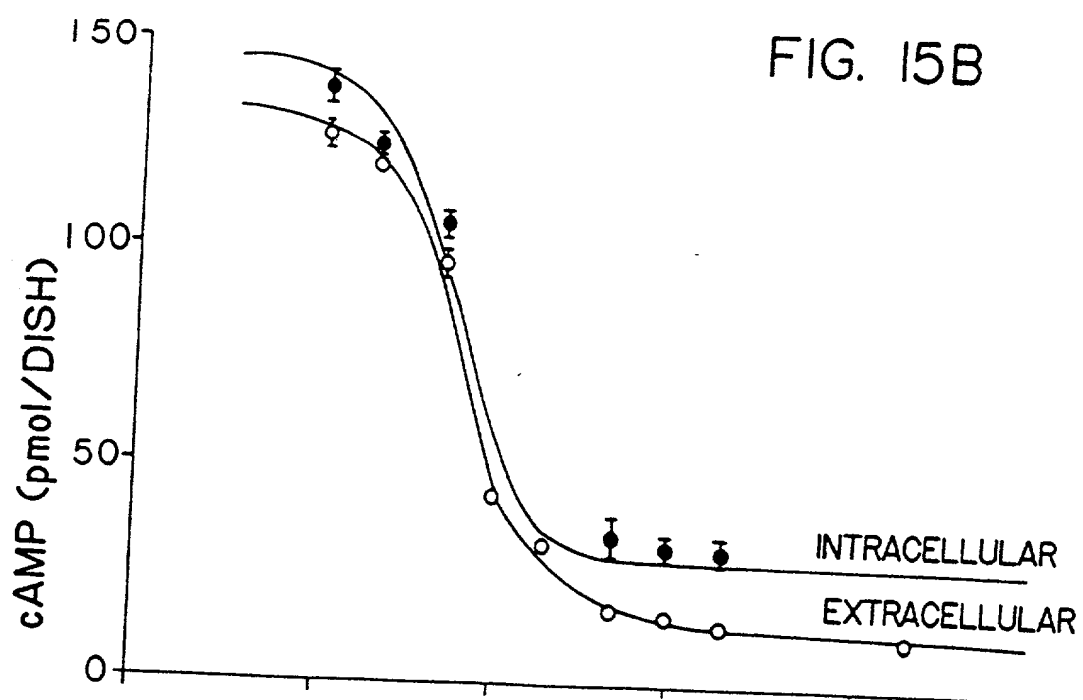
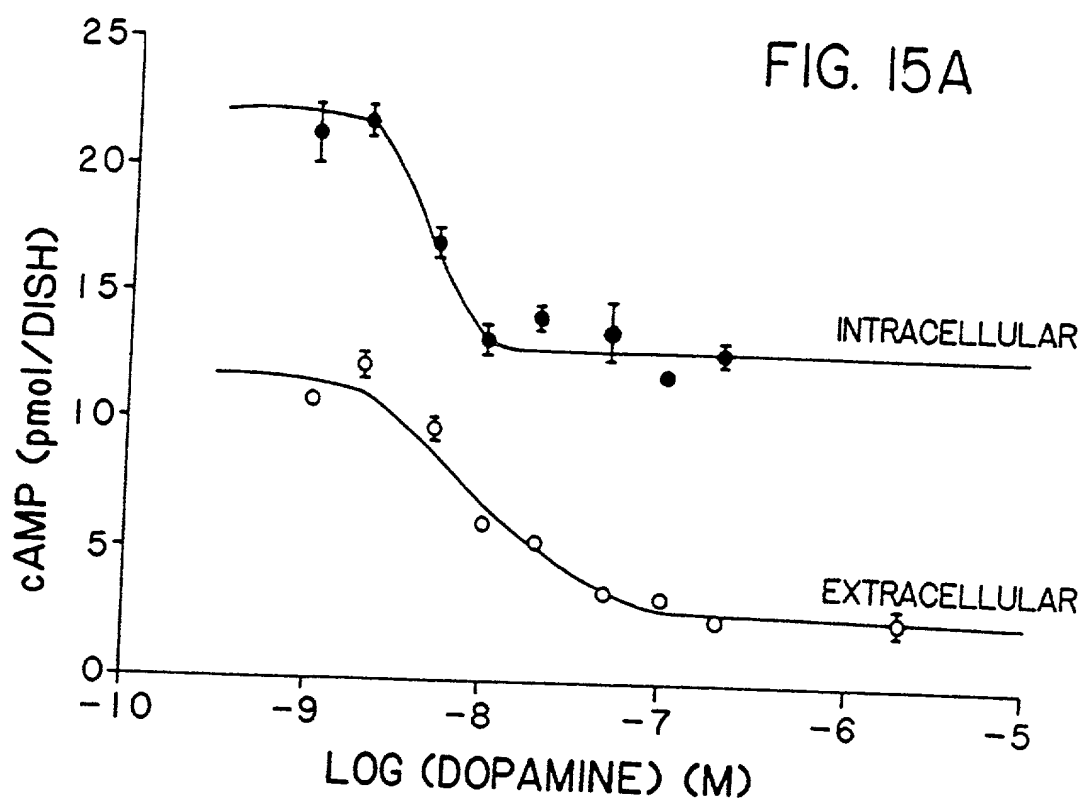


FIG.14B





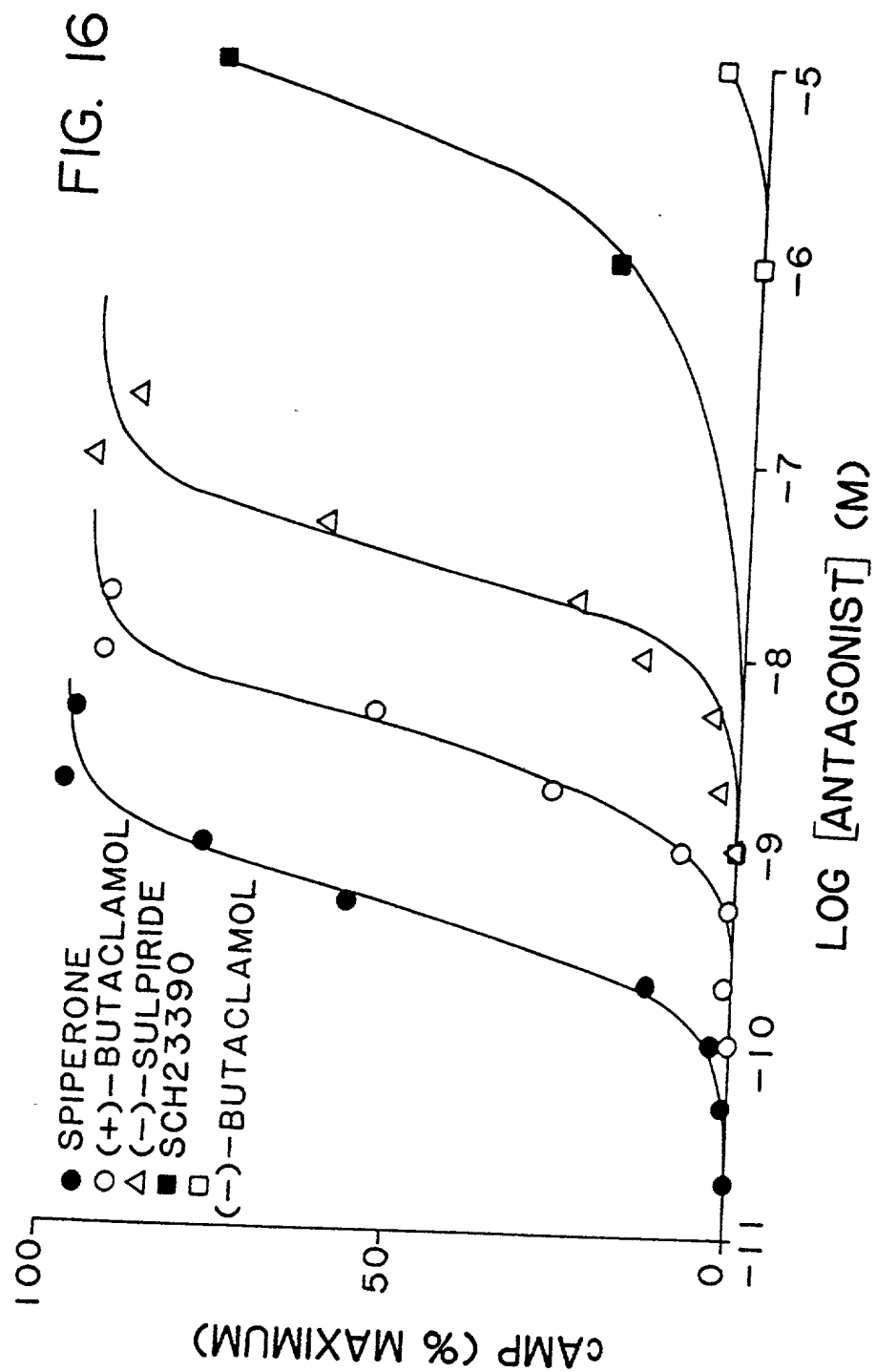


FIG.17A

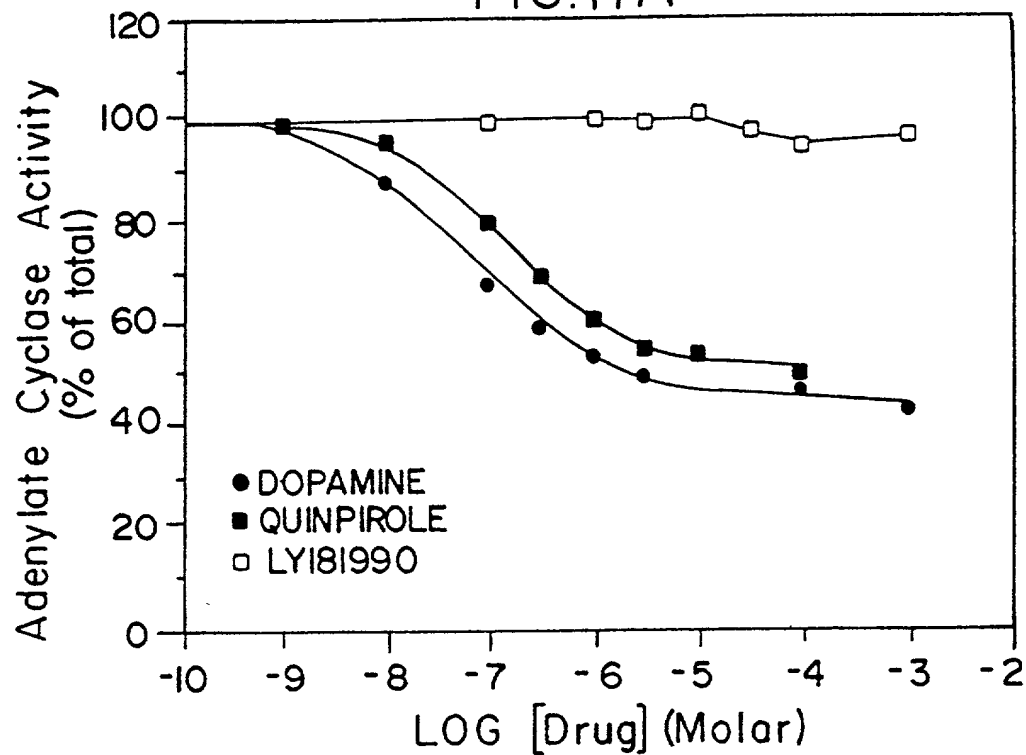
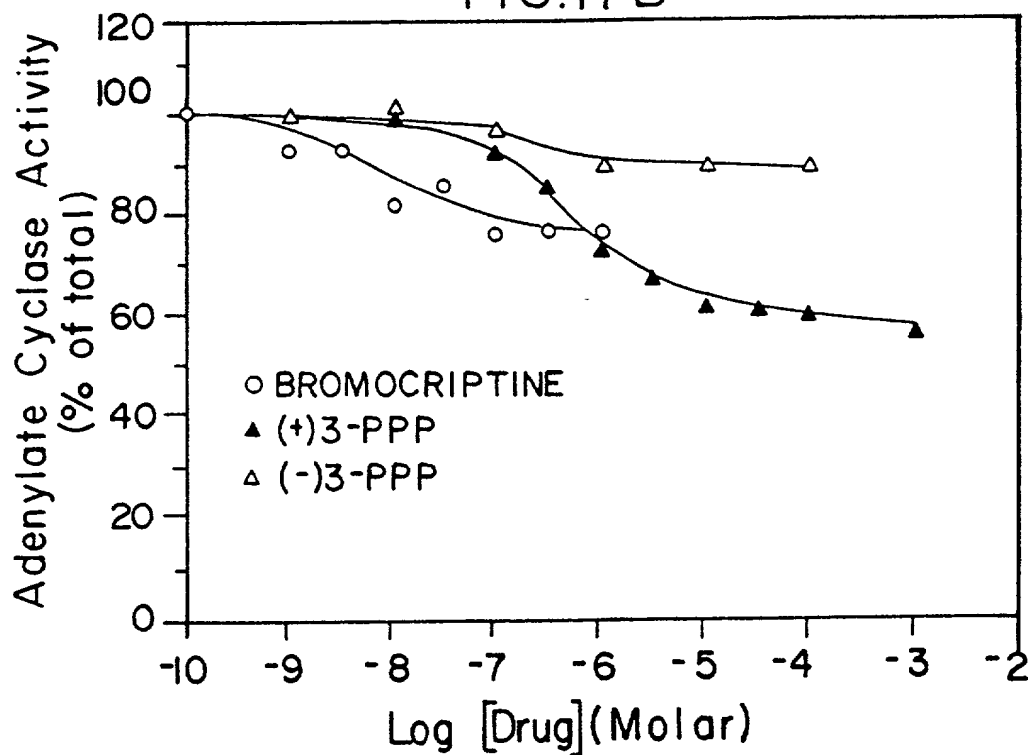


FIG.17B



-33 AGAGCCTGGCCACCCAGTGGTCCACCGCCCTG

[illegible]

*
ProPheAsnGlySerAspGlyLysAlaAspArgProHisTyrAsnTyrTyrAlaThrLeu
30 40
CCCTTCAACGGGTCAGACGGGAAGCGGCAGACCCCACTAACAATACTATGCCACACTG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CCCTTCAATGGGTCAGAAAGGAAGGCAGACAGGCCCACTACAACATACTATGCCATGCTG
Glu
MET

FIG. 18A

1

50

60

LeuThrLeuLeuIleAlaValIleValPheGlyAsnValLeuValCysMETAlaValSer

CTCACCCCTGCTCATCGTCTCTTCGGCAACGTGCTGGTGTGCATGGCTGTGTCC

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

CTCACCCCTCATCTTATCATCGTCTTTGGCAATGTGCTGGTGTGCATGGCTGTATCC

PheIle

70

80

ArgGluLysAlaLeuGlnThrThrThrAsnTyrLeuIleValSerLeuAlaValAlaAsp

CGCGAGAAGCGCTGCAGACCAACCACTACCTGATCGTCAGCCCTCGCAGTGGCCGAC

|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

CGAGAGAAGGCTTTCAGACCAACCACTACTTGATAGTCAGCCTTGCTGTGGCTGAT

240

90

100

LeuLeuValAlaThrLeuValMETProTrpValValTyrLeuGluValValGlyGluTrp

CTCCTCGTCGCCACACTGGTCAATGCCCTGGGTTGTCTACCTGGAGGTGGTAGGTGAGTGG

|| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

CTTCTGGTGGCCACACTGGTAATGCCGTGGGTTGTCTACCTGGAGGTGGTGGGTGAGTGG

FIG. 18B

[illegible]

Ala

IV

ValLeuSerPheThrIleSerCysProLeuLeuPheGlyLeuAsnAsnAlaAspGlnAsn 170 180
 GTCCTGTCCTTCACCATCTCCTGCCCACTCCTCTTCGGACTCAATAACGCAGACCAGAAC
 !!!!!!!
 GTCCTGTCCTTCACCATCTCCTGCCCACTGCTCTTCGGACTCAACAATACAGACCAGAAAT
 Thr

GluCysIleIleAlaAsnProAlaPheValValTyrSerSerIleValSerPheTyrVal 190 200
 V
 GAGTGCATCATTGCCAAACCCGGCCTTCGTGGTCTACTCCTCCATCGTCTCCTTCTACGTG
 !!!!!!!
 GAGTGTATCATTGCCAAACCCCTTGTGGTCTACTCCTCCATTGTCTCATCTACGTG 600

ProPheIleValThrLeuLeuValTyrIleLysIleTyrIleValLeuArgArgArg 210 220
 CCCCTTCATTGTCACCCCTGCTGGTCTACATCAAGATCTACATTGTCTCCGCAGACGCCGC
 !!!!!!!
 CCCCTTCATCGTCACTGCTGCTATATCAAAATCTACATCGTCTCCGGAAGCCCGG
 Lys

FIG. 18D

LysArgValAsnThrLysArgSerSerArgAlaPheArgAlaHisLeuArgAlaProLeu
230 240
AAGCGAGTCAACACCAACGCAGCAGCCGAGCTTTCAGGGGCCACCTGAGGGCTCCACTA
IIIIII IIIIIIIIIII IIIIIIIIIII III IIIIIII I I IIIIIII
AAGCGGTCAACACCAAGCGCAGTCGAGCTTTCAGAGCCCAACCTGAAGACACCACTC
Asn LysThr

*
 LysGlyAsnCysThrHisProGluAspMETLysLeuCysThrValIleMETLysSerAsn
 250
 *
 ▼ AAGGCAACTGTACTACCCCGAGGACATGAAACTCTGCACCGTTATCATGAAGTCTAAT
 !!!
 AAG.....

270 280
GlySerPheProValAsnArgArgValGluAlaAlaArgArgAlaGlnGluLeuGlu
GGGAGTTTCCAGTGAACAGCGGAGAGTGGAGGCTGCCCGCGAGCCCAAGAGCTGGAG
|| ||||| ||||| ||||| ||||| ||||| |||||
.....GATGCTGCCCGCGAGCTCAGGAGCTGGAA
Asp

FIG. 18E

METGluMETLeuSerSerThrSerProProGluArgThrArgTyrSerProIleProPro	290	300
ATGGAGATGCTCTCCAGCACCAAGCCACCCGAGAGAGACCCGGTACAGCCCCATCCCAACC		
IIIIIIIIII II IIIIIIIIIII II IIIIIIIIIII IIIIIIIIIII III		
ATGGAGATGCTGTCAAGCACCAAGCCCCAGAGAGAGACCCGGTATAGCCCATCCCTCCC		
SerHisHisGlnLeuThrLeuProAspProSerHisHisGlyLeuHisSerThrProAsp	310	320
AGCCACCACCACTCTCCCCGACCCGTCCTCCACCATGGTCTCCACAGCACTCCCGAC		
II IIIIIIIIIII IIIIIIIII II IIIIIIIII II IIIIIII III III		960
AGTCACCACCACTCTCCCTGATCCATCCACCAACGGCCTACATAGCAACCCCTGAC		Asn
SerProAlaLysProGluLysAsnGlyHisAlaLys AspHisProLysIleAlaLys	330	339
AGCCCCGCCAAACCAAGAGAAATGGGCATGCCAAA...GACCAACCCCAAGATTGCCAAG		
II II IIIIIIIIIIIIIIIIIIIII IIIII II IIIIIIIIIIIIIIIIIIIII		
AGTCCTGCCAAACCAAGAGAAATGGGCACGCCCAAGATTGTCAATCCCAGGATTGCCAAG		
IleValAsn Arg		

FIG. 18F

IlePheGluIleGlnThrMETProAsnGlyLysThrArgThrSerLeuLysThrMETSer
 ATCTTTGAGATCCAGACCATGCCCAATGGCAAACC CGACCTCCCTCAAGACCATGAGC
 TTTCTTTGAGATCCAGACCATGCCCAATGGCAAACC CGACCTCCCTTAAGACCATGAGC
 phe

[illegible][illegible]

FIG. 18G

AspCysAsnIleProProValLeuTyrSerAlaPheThrTrpLeuGlyTyrValAsnSer
 409 VII 419

GACTGCAACATCCCGCCTGTCTGTACAGCGCCTTCACGTGGCTGGGCTATGTCAACAGC
 II IIIIIIIIIII IIIII IIIIIIIIIII IIIIIIIIIIIII IIIIIIIIIIIII
 GATTGCAACATCCACCAAGTCCTCTACAGCGCCTTCACATGGCTGGCTATGTCAACAGT

AlaValAsnProIleIleTyrThrThrPheAsnIleGluPheArgLysAlaPheLeuLys
 429 439

GCCGTGAACCCCATCATCTACACCACTTCAACATTGAGTTCGCAAGGCCTTCCTGAAG
 IIIII III
 GCCGTCAACCCCATCATCTACACCACTTCAACATCGAGTTCGCAAGGCCTTCATGAAG
 1317
 IleLeuHisCys *
 MET

ATCCTCCACTGCTGACTCTGCTGCCCTGCCCGCACAGCAGCCTGCTTCCCACCTCCCTGCC
 IIII I IIIIIIIIIII
 ATCTTGCACTGCTGA

FIG. 18H

CAGGCGGCCAGCCTCACCCCTTGCGAACCGTGAGCAGGAAGGCCCTGGGTGGATCGGCCCTC 1437

CTCTTCTTAGCCCCGGCAGGCCCTGCAGTGTTGCTTGGCTCCATGCTCCTCACTGCCCG

CACACCCTCACTCTGCCAGGGCAGTGCTAGTGAGCTGGGCATGGTACCAGCCCTGGGGCT 1557

GGCCCCAGCTCAGGGCAGCTCATAGAGTCCCCCTCCACCTCCAGTCCCCCTATCCTT

GGACCAAGATGCAGCGCCTTCCTTGACCTTCCTCTGGGGCTCTAGGGTTGCTGGAGC 1677

CTGAGTCAGGGCCACAGGCTGAGTTTCTCTTTGTGGGGCTTGGCGTGGAGCAGCGGT

GGGAGAGATGGACAGTTCACACCCCTGCAAGGCCACAGGAGCAAGCAAGCTCTTGC 1797

CGAGGAGCCAGGCAACTTCAGTCTGGGAGACCCATGTAAATACCAGACTGCAGTTGGA

CCCCAAGGATTCCCAAGCCAAAACCTTAGCTCCCTCCCGCACCCCGATGTGGACCTCTA 1917

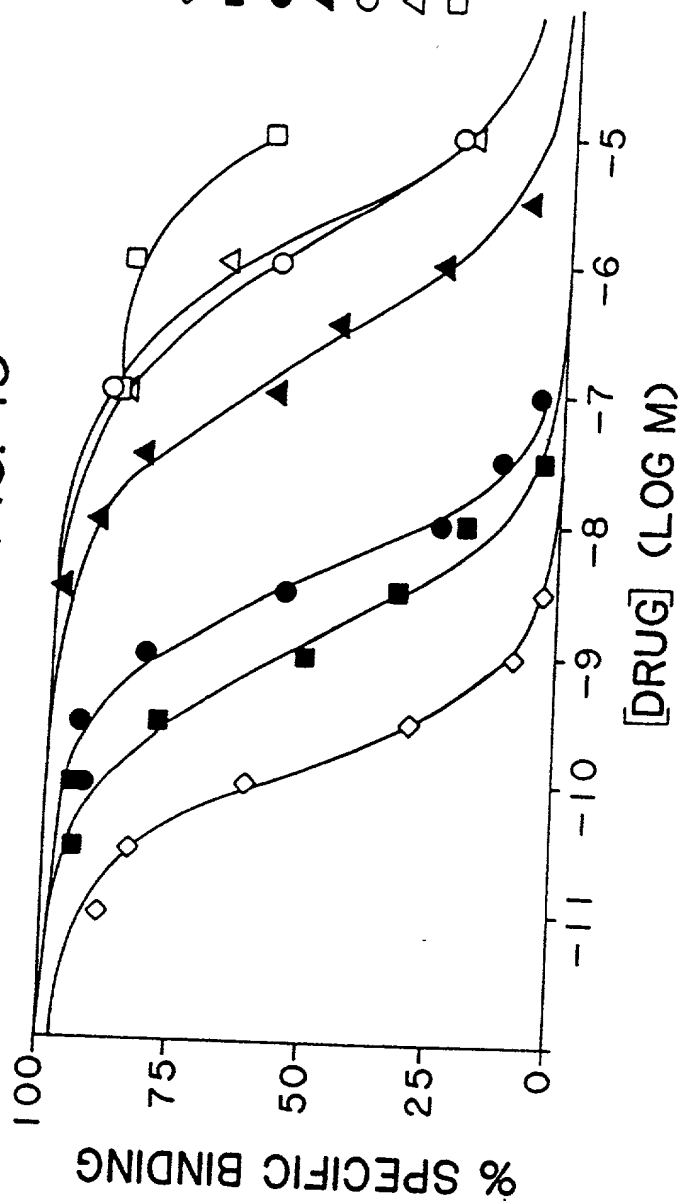
FIG. 18I

CTTCCAGGCTAGTCCGGACCCACCTCACCCCGTTACAGCTCCCAAGTGGTTCCACAT
GCTCTGAGAAGAGGCCCTCATCTTGAAGGCCAGGAGGCTCTATGGGAGAGGAACT 2037
CCTTGGCCTAGCCCACCCCTGCTGCCTTCTGACGGCCCTGCAATGTATCCCTTCTCACAGC
ACATGCTGGCCAGCCTGGGGCCTGGCAGGAGGTCAGGCCCTGGAACCTATCTGGGCCT 2157
GGCTAGGACATCAGAGGTTCTTTGAGGACTGCCCTCTGCCACACTCTGACGCCAAAACC
ACTTCCCTTTCTATTCCCTTCTGGCCTTTCCCTCTCCTGTTTCCCTTCCCTCCACTGC 2277
CTCTGCCCTTAGAGGAGCCACGGCTAAGAGGCTGCTGAAACCATCTGGCCTGGCCTGGC
CCTGCCCTGAGGAAGGAGGCAAGCTGCAGCTTGGGAGAGCCCCTGGGCCTAGACTCTG 2397
TAACATCACTATCCGATGCACCAACTAATAAACTTTGACGAGTCACCTTC (A)_n 2449

FIG. 18J

- ◇ SPIPERONE
- (+)BUTACLAMOL
- HALOPERIDOL
- ▲ SULPIRIDE
- MIANSERIN
- △ SCH-23390
- (-)BUTACLAMOL

FIG. 19



1 2 3 4

kb

—12.0

— 6.0

— 4.0

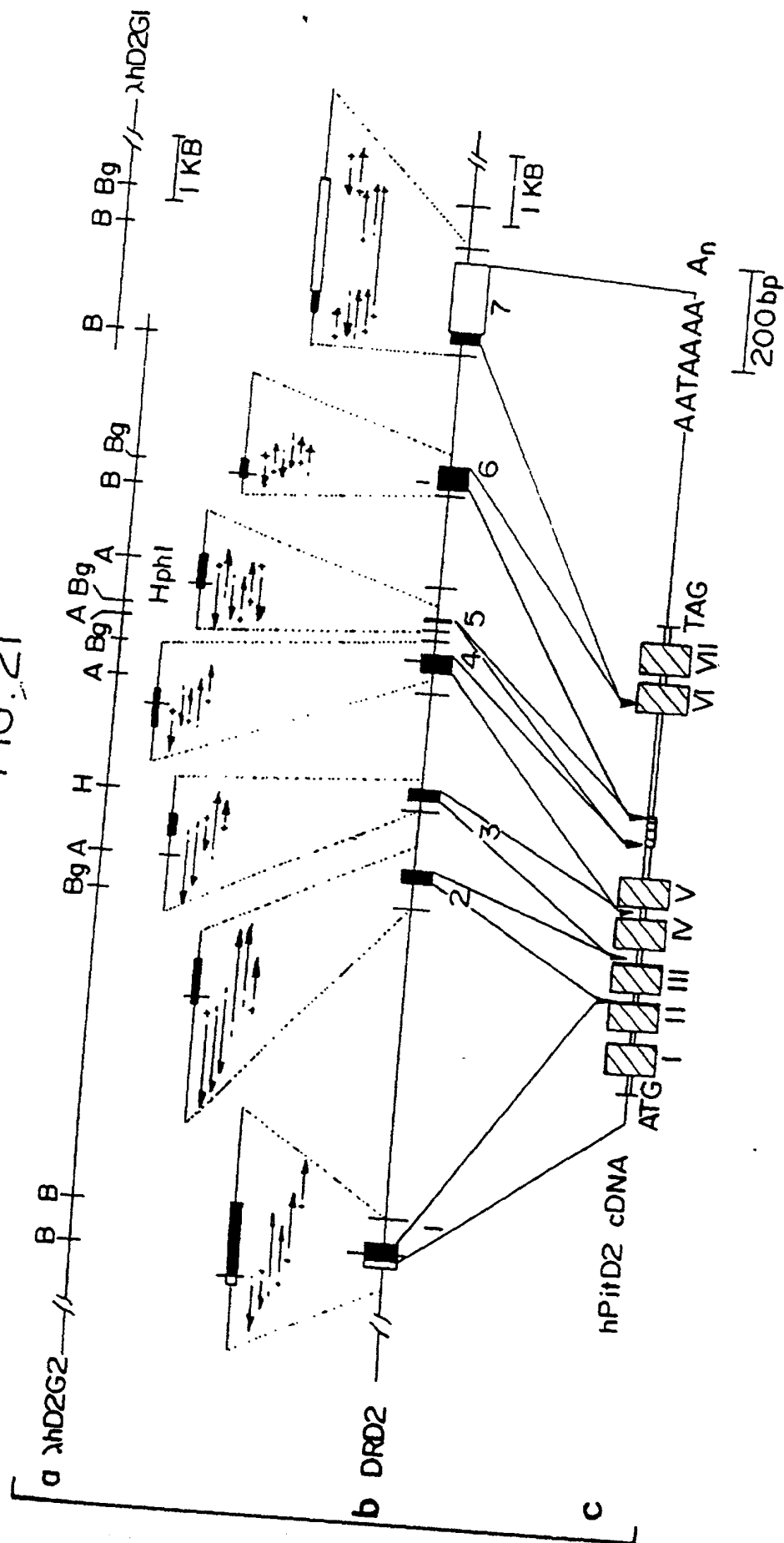
— 2.0

— 1.6

— 1.0

FIG. 20

FIG. 21



DRUG	HUMAN D ₂	RAT D ₂	RAT STRIATUM
SPIPERONE	0.125	0.35	0.56
(+) BUTACLAMOL	0.94	1.2	1.6
HALOPERIDOL	2.4	5.1	5.8
SULPIRIDE	206	160	205
MIANSERIN (5-HT)	2685	4300	4600
SCH 23390 (DI)	2145	2500	3300
(+) BUTACLAMOL	>10,000	>10,000	>10,000
Kd [³ H] DOMPERIDONE	0.74	0.40	0.40

FIG. 22

FIG. 23

2851	286
exon1...GGA [.] Gtagtg...intron1...tccccagGTGG...exon2	
395	396
exon2...ACA [.] Ggtgagcc...intron2...cttgcagGTAC...exon3	
532	533
exon3...GCA [.] Ggtacatt...intron3...ccccccagACCA...exon4	
723	724
exon4...AAA [.] Ggtctcaa...intron4...tccacagGGCA...exon5	
810	811
exon5...AGT [.] Ggtaagt...intron5...gggtcagGAGG...exon6	
1138	1139
exon6...CTC [.] Ggtgagtc...intron6...ccccccagGCGT...exon7	

¹Numbering begins with A of the putative initiator methionine codon (see Fig. 18)